

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: July 27, 2005, 03:27:05 ; Search time 43 Seconds
(without alignments)

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Title: US-09-502-176-2
Perfect score: 1540
Sequence: 1 VYLSCKTGKNGKNGVYRTGMSK.....TNSQVRWBYCKIPSQCDSSPV 260

Scoring table: Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents AA:
1: /cgns_6/prodata/1/iaa/5A.COMB.pep:
2: /cgns_6/prodata/1/iaa/5B.COMB.pep:
3: /cgns_6/prodata/1/iaa/6A.COMB.pep:
4: /cgns_6/prodata/1/iaa/6B.COMB.pep:
5: /cgns_6/prodata/1/iaa/PCFTUS.COMB.pep:
6: /cgns_6/prodata/1/iaa/backfile1.pep:
APPLICANT: Maden, John

APPLICANT: Liang, Hong

APPLICANT: Sim, Kim Lee

APPLICANT: Zhou, Xinhua

APPLICANT: Chang-Murad, Amy

APPLICANT: Boerner, Renee J.

APPLICANT: Bermejo, Lourdes L.

APPLICANT: Misry, Firoz R.

APPLICANT: Schrimsher, Jeffrey L.

PRED. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1540	100.0	260	4 US-09-982-516-1 Sequence 1, Appli
2	1535	99.7	339	1 US-08-248-629A-3 Sequence 3, Appli
3	1535	99.7	339	1 US-08-51-922-3 Sequence 3, Appli
4	1535	99.7	339	1 US-08-452-20-3 Sequence 3, Appli
5	1535	99.7	339	1 US-08-326-575-3 Sequence 3, Appli
6	1535	99.7	339	2 US-08-12-708-3 Sequence 3, Appli
7	1535	99.7	339	2 US-08-05-588B-3 Sequence 3, Appli
8	1535	99.7	339	2 US-08-429-733-3 Sequence 3, Appli
9	1535	99.7	339	2 US-08-866-735-3 Sequence 3, Appli
10	1535	99.7	339	3 US-09-066-028-3 Sequence 3, Appli
11	1535	99.7	339	4 US-03-335-325-3 PCT-US5-0507-3
12	1535	99.7	339	5 PCT-US5-0507-3
13	1535	99.7	374	3 US-09-377-250-3 Sequence 3, Appli
14	1535	99.7	375	3 US-09-377-250-4 Sequence 3, Appli
15	1535	99.7	378	2 US-08-612-088-42 Sequence 4, Appli
16	1535	99.7	378	3 US-09-066-028-42 Sequence 4, Appli
17	1535	99.7	378	4 US-08-055-1 Sequence 4, Appli
18	1535	99.7	378	4 US-09-335-325-42 Sequence 4, Appli
19	1535	99.7	451	3 US-09-377-250-1 Sequence 4, Appli
20	1535	99.7	452	3 US-09-377-250-4 Sequence 4, Appli
21	1535	99.7	790	1 US-08-469-466-54 Sequence 5, Appli
22	1535	99.7	790	2 US-08-469-558-54 Sequence 5, Appli
23	1535	99.7	791	1 US-08-643-219-1 Sequence 1, Appli
24	1535	99.7	791	2 US-09-131-915-1 Sequence 1, Appli
25	1535	99.7	791	2 US-08-832-087B-1 Sequence 1, Appli
26	1535	99.7	791	3 US-08-851-350-1 Sequence 1, Appli
27	1535	99.7	791	3 US-09-132-154-1 Sequence 1, Appli

ALIGNMENTS

28	1535	99.7	791	4 US-08-991-761A-6 Sequence 6, Appli
29	1535	99.7	791	4 US-08-924-287A-1 Sequence 1, Appli
30	1535	99.7	810	1 US-07-854-603-2 Sequence 2, Appli
31	1535	99.7	810	1 US-08-147-008B-29 Sequence 29, Appli
32	1535	99.7	810	3 US-09-086-514-1 Sequence 1, Appli
33	1535	99.7	810	4 US-09-192-012-5 Sequence 5, Appli
34	1535	99.7	810	4 US-09-403-736-1 Sequence 1, Appli
35	1535	99.7	810	4 US-09-701-265-1 Sequence 1, Appli
36	1535	99.7	814	1 US-08-750-711-1 Sequence 1, Appli
37	1532	99.5	713	4 US-09-949-016-983 Sequence 993, Appli
38	1531	99.4	369	4 US-09-701-265-2 Sequence 2, Appli
39	1531	99.4	810	6 5200340-8 Patent No. 5200340
40	1531	99.4	810	6 5200340-8 Patent No. 5200340
41	1511	98.1	352	2 US-08-612-788-40 Sequence 40, Appli
42	1511	98.1	352	3 US-09-066-028-40 Sequence 40, Appli
43	1511	98.1	352	4 US-03-335-25-40 Sequence 3, Appli
44	1505	97.7	254	4 US-09-701-265-3 Sequence 30, Appli
45	1486	96.5	250	2 US-08-612-788-30 Sequence 30, Appli

Qy 241 TNSQVRWEYCKIPSCDSSPV 260

Db 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 2
US-08-248-629A-3
; Sequence 3, Application US/08248629A

; Patent No. 5639725

; GENERAL INFORMATION:

; APPLICANT: Folkman, Judah

; APPLICANT: O'Reilly, Michael

; TITLE OF INVENTION: Method of Treating an Angiogenic

; TITLE OF INVENTION: Disease

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Jones & Askew

; STREET: 191 Peachtree Street, 37th Floor

; CITY: Atlanta

; STATE: Georgia

; COUNTRY: USA

; ZIP: 30303-1769

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50

; COMPUTER: Macintosh

; OPERATING SYSTEM: 7.0

; SOFTWARE: Microsoft Word

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/248,629A

; FILING DATE: 04/26/94

; CLASSIFICATION: 514

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: 04/26/94

; ATTORNEY/AGENT INFORMATION:

; NAME: Larry W. Stults, Ph.D.

; REFERENCE/DOCKET NUMBER: 34,025

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 404-818-3700

; FAX: 404-818-3799

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 339

; TYPE: amino acid

; TOPOLOGY: linear

US-08-248-629A-3

RESULT 3
US-08-451-932-3

; Sequence 3, Application US/08451932

; Patent No. 5733876

; GENERAL INFORMATION:

; APPLICANT: O'Reilly, Michael

; TITLE OF INVENTION: Method of Treating an Angiogenic

; TITLE OF INVENTION: Disease

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Jones & Askew

; STREET: 191 Peachtree Street, 37th Floor

; CITY: Atlanta

; STATE: Georgia

; COUNTRY: USA

; ZIP: 30303-1769

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50

; COMPUTER: Macintosh

; OPERATING SYSTEM: 7.0

; SOFTWARE: Microsoft Word

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/451,932

; FILING DATE: 05/26/95

; CLASSIFICATION: 514

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: 08/248,629

; ATTORNEY/AGENT INFORMATION:

; NAME: Larry W. Stults, Ph.D.

; REFERENCE/DOCKET NUMBER: 34,025

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 404-818-3700

; FAX: 404-818-3799

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 339

; TYPE: amino acid

; TOPOLOGY: linear

US-08-451-932-3

Query Match 99.7%; Score 1535; DB 1; Length 339;

Best Local Similarity 99.6%; Pred. No. 1.4e-138; Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VYLSBECKTGNGKRYGRTMSKTKNGTICQKNSSTSPPHRPRFSPATHPSSEGLHENYCRNPDN 60

Db 1 VYLSBECKTGNGKRYGRTMSKTKNGTICQKNSSTSPPHRPRFSPATHPSSEGLHENYCRNPDN 60

Qy 61 DRQGPCKYTDPERKVDYCOLLEBECMCSGENYDGKISKTMISGLEQAWDSOPHAR 120

Db 61 DRQGPCKYTDPERKVDYCOLLEBECMCSGENYDGKISKTMISGLEQAWDSOPHAR 120

Qy 121 GYIPSKFPKNLKKVCRNPDRELPWCFTDPNKRWELCDIPRCTTPSSGPTYOCLK 180

Db 121 GYIPSKFPKNLKKVCRNPDRELPWCFTDPNKRWELCDIPRCTTPSSGPTYOCLK 180

Qy 181 GTGENTRGNVAVTSGHTCOHWSAQTPHTNRPENFPCKNLDENYCRNPDKRAPWCT 240

Db 181 GTGENTRGNVAVTSGHTCOHWSAQTPHTNRPENFPCKNLDENYCRNPDKRAPWCT 240

Qy 181 GTGENTRGNVAVTSGHTCOHWSAQTPHTNRPENFPCKNLDENYCRNPDKRAPWCT 240

Db 143 GTGENTRGNVAVTSGHTCOHWSAQTPHTNRPENFPCKNLDENYCRNPDKRAPWCT 240

Qy 241 TNSQVRWEYCKIPSCDSSPV 260

Db 241 TNSQVRWEYCKIPSCDSSPV 260

; RESULT 4
US-08-452-260-3

; Sequence 3, Application US/08452260

; Patent No. 5776704

; GENERAL INFORMATION:

APPLICANT: Folkmann, Judah
 TITLE OF INVENTION: Method of Diagnosing an Angiogenic
 NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Jones & Askew
 STREET: 191 Peachtree Street, 37th Floor
 CITY: Atlanta
 STATE: Georgia
 COUNTRY: USA
 ZIP: 30303-1769

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50
 COMPUTER: Macintosh
 OPERATING SYSTEM: 7.0
 SOFTWARE: Microsoft Word

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/452,260
 FILING DATE: 05/25/95
 CLASSIFICATION: 514
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/248,629
 FILING DATE: 09/26/94
 ATTORNEY/AGENT INFORMATION:
 NAME: Larry W. Stults, Ph.D.
 REGISTRATION NUMBER: 34,025
 REFERENCE/DOCKET NUMBER: 05213-0124

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 404-818-3700
 TELEX/FAX: 404-818-3799

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
 LENGTH: 339
 TYPE: amino acid
 TOPOLOGY: linear
 US-08-452-260-3

Query Match 99.7%; Score 1535; DB 1; Length 339;
 Best Local Similarity 99.6%; Pred. No. 1.4e-138;
 Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VYLSECKTGNGKNGYRGTMKTRGTTGKQWKSSTSPHRPFSRATHPSGLEENYCRNPDN 60
 Db 1 VYLSECKTGNGKNGYRGTMKTRGTTGKQWKSSTSPHRPFSRATHPSGLEENYCRNPDN 60

Qy 61 DPGQPKWYTYDPEKRYDQYCDLCECERCMHSGENYDGKISKTMMSGLGQAMQSOPHAK 120
 Db 61 DPGQPKWYTYDPEKRYDQYCDLCECERCMHSGENYDGKISKTMMSGLGQAMQSOPHAK 120

Qy 121 GYIPSKPNKLNKQNYCPRDPDRTRPWFETTDPKRWECDIRCTTPPPSSGPTYQCLK 180
 Db 121 GYIPSKPNKLNKQNYCPRDPDRTRPWFETTDPKRWECDIRCTTPPPSSGPTYQCLK 180

Qy 181 GTGENYRGNAVTVSIGHTCOHWSAQTOPHTHERTPENFCKNLDENYCRNPDGKRAPWHT 240
 Db 181 GTGENYRGNAVTVSIGHTCOHWSAQTOPHTHERTPENFCKNLDENYCRNPDGKRAPWHT 240

Qy 241 TNSQVRWECKIKPSCDSPV 260
 Db 241 TNSQVRWECKIKPSCDSPV 260

RESULT 6
 US-08-612-788-3
 Sequence 3, Application US/08612788
 Patent No. 5837682

GENERAL INFORMATION:
 APPLICANT: Folkmann, M. Judah
 APPLICANT: Cao, Yihai
 APPLICANT: Sim, B. Kim Lee
 TITLE OF INVENTION: Angiotatin Fragments and Method of Use
 NUMBER OF SEQUENCES: 45

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Jones & Askew
 STREET: 191 Peachtree Street, 37th Floor
 CITY: Atlanta
 STATE: Georgia

ADDRESSEE: Jones & Askew
 STREET: 191 Peachtree Street, 37th Floor
 CITY: Atlanta
 STATE: Georgia
 COUNTRY: USA
 ZIP: 30303-1769

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50
 COMPUTER: Macintosh
 OPERATING SYSTEM: 7.0
 SOFTWARE: Microsoft Word

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/326,785
 FILING DATE: 04/26/94
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Larry W. Stults, Ph.D.
 REGISTRATION NUMBER: 34,025
 REFERENCE/DOCKET NUMBER: 05213-0124

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 404-818-3700
 TELEX/FAX: 404-818-3799

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
 LENGTH: 339
 TYPE: amino acid
 TOPOLOGY: linear
 US-08-326-785-3

Query Match 99.7%; Score 1535; DB 1; Length 339;
 Best Local Similarity 99.6%; Pred. No. 1.4e-138;
 Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VYLSECKTGNGKNGYRGTMKTRGTTGKQWKSSTSPHRPFSRATHPSGLEENYCRNPDN 60
 Db 1 VYLSECKTGNGKNGYRGTMKTRGTTGKQWKSSTSPHRPFSRATHPSGLEENYCRNPDN 60

Qy 61 DPGQPKWYTYDPEKRYDQYCDLCECERCMHSGENYDGKISKTMMSGLGQAMQSOPHAK 120
 Db 61 DPGQPKWYTYDPEKRYDQYCDLCECERCMHSGENYDGKISKTMMSGLGQAMQSOPHAK 120

Qy 121 GYIPSKPNKLNKQNYCPRDPDRTRPWFETTDPKRWECDIRCTTPPPSSGPTYQCLK 180
 Db 121 GYIPSKPNKLNKQNYCPRDPDRTRPWFETTDPKRWECDIRCTTPPPSSGPTYQCLK 180

Qy 181 GTGENYRGNAVTVSIGHTCOHWSAQTOPHTHERTPENFCKNLDENYCRNPDGKRAPWHT 240
 Db 181 GTGENYRGNAVTVSIGHTCOHWSAQTOPHTHERTPENFCKNLDENYCRNPDGKRAPWHT 240

Qy 241 TNSQVRWECKIKPSCDSPV 260
 Db 241 TNSQVRWECKIKPSCDSPV 260

COUNTRY: U.S.
 ZIP: 30303-1769
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/612,788
 FILING DATE:
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Warren, William L.
 REFERENCE/DOCKET NUMBER: 36,714
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 404-818-3700
 TELEX/FAX: 404-818-3799
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 339 amino acids
 TYPE: amino acid
 ORGANISM: Homo sapiens
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: N-terminal
 ORIGINAL SOURCE:
 IMMEDIATE SOURCE:
 CLONE: Angiostatin fragment
 ; US-08-612-788-3

Query Match 99.7%; Score 1535; DB 2; Length 339;
 Best Local Similarity 99.6%; Pred. No. 1.4e-138; Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VYLSCKTGNGKVRGTMKTKGTCQKWSSTSPPHRPSPATHSEGLENTCRNPDN 60
 Db 1 VYLSCKTGNGKVRGTMKTKGTCQKWSSTSPPHRPSPATHSEGLENTCRNPDN 60

Qy 61 DPGCPWCYTDPERKRYDQCLLCEBECMHCSGENYDGKISKTMGLCQAWDSOPRAH 120
 Db 61 DPGCPWCYTDPERKRYDQCLLCEBECMHCSGENYDGKISKTMGLCQAWDSOPRAH 120

Qy 121 GYIPSKEPNKNLKKNYCRNPRELRCFTDPNRPWELCDIPRTTPPSGGTYQCLK 180
 Db 121 GYIPSKEPNKNLKKNYCRNPRELRCFTDPNRPWELCDIPRTTPPSGGTYQCLK 180

Qy 181 GTGGENYRGNVAVTSGHTCQHSAQTPTHTPENPCQNDENYCRPDGKRAPWCH 240
 Db 181 GTGGENYRGNVAVTSGHTCQHSAQTPTHTPENPCQNDENYCRPDGKRAPWCH 240

Qy 241 TNSQVRWEYCKIPSCDSSPV 260
 Db 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 7
 US-08-605-598B-3
 Sequence 3, Application US/08605598B
 Patent No. 5885795
 GENERAL INFORMATION:
 APPLICANT: Folkman, M. Judah
 APPLICANT: Lin, Jie
 APPLICANT: O'Reilly, Michael S.
 TITLE OF INVENTION: Aggregate Angiostatin and Method of Use
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Jones & Askew
 STREET: 191 Peachtree Street, 37th Floor
 CITY: Atlanta
 STATE: Georgia
 COUNTRY: U.S.
 ZIP: 30303-1769

STATE: Georgia
 COUNTRY: U.S.
 ZIP: 30303-1769
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/605,598B
 FILING DATE: 22-FEB-1995
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Warren, William L.
 REFERENCE/DOCKET NUMBER: 36,714
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 404-818-3700
 TELEX/FAX: 404-818-3799
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 339 amino acids
 TYPE: amino acid
 ORGANISM: Human Angiostatin
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide
 ORIGINAL SOURCE:
 US-08-605-598B-3

Query Match 99.7%; Score 1535; DB 2; Length 339;
 Best Local Similarity 99.6%; Pred. No. 1.4e-138; Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VYLSCKTGNGKVRGTMKTKGTCQKWSSTSPPHRPSPATHSEGLENTCRNPDN 60
 Db 1 VYLSCKTGNGKVRGTMKTKGTCQKWSSTSPPHRPSPATHSEGLENTCRNPDN 60

Qy 61 DPGCPWCYTDPERKRYDQCLLCEBECMHCSGENYDGKISKTMGLCQAWDSOPRAH 120
 Db 61 DPGCPWCYTDPERKRYDQCLLCEBECMHCSGENYDGKISKTMGLCQAWDSOPRAH 120

Qy 121 GYIPSKEPNKNLKKNYCRNPRELRCFTDPNRPWELCDIPRTTPPSGGTYQCLK 180
 Db 121 GYIPSKEPNKNLKKNYCRNPRELRCFTDPNRPWELCDIPRTTPPSGGTYQCLK 180

Qy 181 GTGGENYRGNVAVTSGHTCQHSAQTPTHTPENPCQNDENYCRPDGKRAPWCH 240
 Db 181 GTGGENYRGNVAVTSGHTCQHSAQTPTHTPENPCQNDENYCRPDGKRAPWCH 240

Qy 241 TNSQVRWEYCKIPSCDSSPV 260
 Db 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 8
 US-08-429-743-3
 Sequence 3, Application US/08429743
 Patent No. 5885795
 GENERAL INFORMATION:
 APPLICANT: O'Reilly, Michael
 APPLICANT: Folkman, M. Judah
 APPLICANT: Sim, Kim Lee
 APPLICANT: Cao, Yihai
 TITLE OF INVENTION: Angiostatin and Method of Use
 NUMBER OF SEQUENCES: 6
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Jones & Askew
 STREET: 191 Peachtree Street, 37th Floor
 CITY: Atlanta
 STATE: Georgia
 COUNTRY: U.S.
 ZIP: 30303-1769

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATOR: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA: US/08/429, 743

FILING DATE: 26-APR-1994

CLASSIFICATION: 424

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 08/248, 629

REGISTRATION NUMBER: 31,771

REFERENCE/DOCKET NUMBER: 05213-0122

TELECOMMUNICATION INFORMATION:

TELEPHONE: (404) 818-3700

TELEFAX: (404) 818-3799

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS: LENGTH: 339 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: N-terminal

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

IMMEDIATE SOURCE:

CLONE: Angiotensin fragment

US-08-429-743-3

Query Match 99.7%; Score 1535; DB 2; Length 339; Best Local Similarity 99.6%; Pred. No. 1.4e-138; Matches 259; Conservativeness 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VYLSECKTGNGKNGYRGTMKSTKGITGKTSKTMGLCOWDSDOPAH Db 1 DPOGPWCYTDPKRYCDILCEBECMHSGENTDGKTSKTMGLCOWDSDOPDN

Qy 61 DPOGPWCYTDPKRYCDILCEBECMHSGENTDGKTSKTMGLCOWDSDOPAH Db 61 DPOGPWCYTDPKRYCDILCEBECMHSGENTDGKTSKTMGLCOWDSDOPAH

Qy 121 GYISKPKNLKKNYCRNPDRLRPWTIDDKRKLWCLDIPRCTTPPPSSGTYQLK Db 121 GYISKPKNLKKNYCRNPDRLRPWTIDDKRKLWCLDIPRCTTPPPSSGTYQLK

Qy 181 GTGENYRGNVAVTVSGHTCQHWSAQTPHTHERTPENPPCKLQDENYCRNPDRGKRAPWHT Db 181 GTGENYRGNVAVTVSGHTCQHWSAQTPHTHERTPENPPCKLQDENYCRNPDRGKRAPWHT

Qy 241 TNSQVRWEYCKIPSCDSSPV Db 241 TNSQVRWEYCKIPSCDSSPV

Qy 241 TNSQVRWEYCKIPSCDSSPV Db 241 TNSQVRWEYCKIPSCDSSPV

RESULT 9
US-01-866-735-3

Sequence 3, Application US/08866735

Patent No. 595403

GENERAL INFORMATION:

APPLICANT: Folkman, M. Judah

TITLE OF INVENTION: Angiotatin Fragments and Method of Use

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Jones & Askew, LLP

STREET: 191 Peachtree Street, 37th Floor

CITY: Atlanta
STATE: Georgia

COUNTRY: USA

ZIP: 30303-1769

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATOR: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA: US/09/066028

FILING DATE: 30-MAY-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Warren, William L.

REGISTRATION NUMBER: 3, 714

REFERENCE/DOCKET NUMBER: 05940-0129

TELECOMMUNICATION INFORMATION:

TELEPHONE: (404) 818-3700

TELEFAX: (404) 818-7799

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS: LENGTH: 339 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: N-terminal

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

IMMEDIATE SOURCE:

CLONE: Angiotatin fragment

Query Match 99.7%; Score 1535; DB 2; Length 339; Best Local Similarity 99.6%; Pred. No. 1.4e-138; Matches 259; Conservativeness 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VYLSECKTGNGKNGYRGTMKSTKGITGKTSKTMGLCOWDSDOPAH Db 1 DPOGPWCYTDPKRYCDILCEBECMHSGENTDGKTSKTMGLCOWDSDOPDN

Qy 61 DPOGPWCYTDPKRYCDILCEBECMHSGENTDGKTSKTMGLCOWDSDOPAH Db 61 DPOGPWCYTDPKRYCDILCEBECMHSGENTDGKTSKTMGLCOWDSDOPAH

Qy 121 GYISKPKNLKKNYCRNPDRLRPWTIDDKRKLWCLDIPRCTTPPPSSGTYQLK Db 121 GYISKPKNLKKNYCRNPDRLRPWTIDDKRKLWCLDIPRCTTPPPSSGTYQLK

Qy 181 GTGENYRGNVAVTVSGHTCQHWSAQTPHTHERTPENPPCKLQDENYCRNPDRGKRAPWHT Db 181 GTGENYRGNVAVTVSGHTCQHWSAQTPHTHERTPENPPCKLQDENYCRNPDRGKRAPWHT

Qy 241 TNSQVRWEYCKIPSCDSSPV Db 241 TNSQVRWEYCKIPSCDSSPV

Qy 241 TNSQVRWEYCKIPSCDSSPV Db 241 TNSQVRWEYCKIPSCDSSPV

RESULT 10
US-09-066-028-3

Sequence 3, Application US/09066028

Patent No. 602488

GENERAL INFORMATION:

APPLICANT: Folkman, M. Judah

TITLE OF INVENTION: Angiotatin Fragments and Method of Use

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Jones & Askew, LLP

STREET: 191 Peachtree Street, 37th Floor

CITY: Atlanta
STATE: Georgia

CITY: Atlanta
 STATE: Georgia
 COUNTRY: U.S.
 ZIP: 30303-1769

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/066,028
 FILING DATE:
 CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/612,788
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:

NAME: Warren, William L.
 REGISTRATION NUMBER: 36,714
 REFERENCE/DOCKET NUMBER: 05213-0126
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 404-818-3700
 TELEFAX: 404-818-3799

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 339 amino acids
 TYPE: amino acid
 STRANDEDNESS: linear

MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO

FRAGMENT TYPE: N-terminal
 ORIGINAL SOURCE:

ORGANISM: Homo sapiens
 IMMEDIATE SOURCE:
 CLONE: Angiotatin fragment
 /US-09-066-028-3

Query Match 99.7%; Score 1535; DB 3; Length 339;
 Best Local Similarity 99.6%; Pred. No. 1.4e-138;
 Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLSECKTGNGKNGYRGTMKSKNGITCQKWSSTSPHRPRPFSATHPSEGLENVCRNDN 60
 1 |||||||V|||L|||S|E||C||K|T|G|N|G|K|N|G|Y|R|G|T|M|K|S|K|N|G|I|T|C|Q|K|W|S|S|T|S|P|H|R|P|R|P|F|S|A|T|H|P|S|E|G|L|E|N|V|C|R|N|D|N 60

Db 61 DPGGPWCYTTPDEKRYDCDIECEBECMHCSGENYDGKISKTMMSGLEQAWNSQSOPHAH 120
 1 |||D|P|G|G|P|W|C|Y|T|T|P|D|E|K|R|Y|D|C|D|I|E|C|E|B|E|C|M|H|C|S|G|E|N|Y|D|G|K|I|S|K|T|M|S|G|L|E|Q|A|W|N|S|Q|S|O|P|H|A|H 120

Db 61 DPOGPWCYTTPDEKRYDCDIECEBECMHCSGENYDGKISKTMMSGLEQAWNSQSOPHAH 120
 1 |||D|P|O|G|P|W|C|Y|T|T|P|D|E|K|R|Y|D|C|D|I|E|C|E|B|E|C|M|H|C|S|G|E|N|Y|D|G|K|I|S|K|T|M|S|G|L|E|Q|A|W|N|S|Q|S|O|P|H|A|H 120

QY 121 GYIISKFKNQNLKKQYCRNPDRRELWPWCFTDPNPKWELCDIPRCTPPSSGPTYQCK 180
 1 |||G|Y|I|I|S|K|F|K|N|Q|N|L|K|K|Q|Y|C|R|N|P|D|R|R|E|L|R|W|P|W|C|F|T|D|P|N|P|K|W|E|L|C|D|I|P|R|C|T|T|P|P|S|S|G|P|T|Y|Q|C|K 180

Db 121 GYIISKFKNQNLKKQYCRNPDRRELWPWCFTDPNPKWELCDIPRCTPPSSGPTYQCK 180
 1 |||G|Y|I|I|S|K|F|K|N|Q|N|L|K|K|Q|Y|C|R|N|P|D|R|R|E|L|R|W|P|W|C|F|T|D|P|N|P|K|W|E|L|C|D|I|P|R|C|T|T|P|P|S|S|G|P|T|Y|Q|C|K 180

QY 181 GTGENYRGNVAVTVSGHTCOHWSAQTPHTPRTENPKCQNLDENYCRNPDKRAPWCT 240
 1 |||G|T|G|E|N|Y|R|G|N|V|A|V|T|V|S|G|H|T|C|O|H|W|S|A|Q|T|P|H|T|P|R|T|E|N|P|K|C|Q|N|L|D|E|N|Y|C|R|N|P|D|G|K|R|A|P|W|C|T 240

Db 181 GTGENYRGNVAVTVSGHTCOHWSAQTPHTPRTENPKCQNLDENYCRNPDKRAPWCT 240
 1 |||G|T|G|E|N|Y|R|G|N|V|A|V|T|V|S|G|H|T|C|O|H|W|S|A|Q|T|P|H|T|P|R|T|E|N|P|K|C|Q|N|L|D|E|N|Y|C|R|N|P|D|G|K|R|A|P|W|C|T 240

Qy 241 TNSQVRWECKIPSCDSSPV 260
 1 |||T|N|S|Q|V|R|W|E|C|K|I|P|S|C|D|S|S|P|V 260

Db 241 TNSQVRWECKIPSCDSSPV 260
 1 |||T|N|S|Q|V|R|W|E|C|K|I|P|S|C|D|S|S|P|V 260

RESULT 11

; Sequence 3, Application US/0935325
 Patent No. 652439

GENERAL INFORMATION:

APPLICANT: Folkmann, M. Judah
 O'Reilly, Michael
 Cao, Yilai
 Sim, B. Kim Lee

US-09-335-3325-3

QY 181 GTCENTRGRNVAVTVSGHTCOHWSAQTPHTPRTENPKCQNLDENYCRNPDKRAPWCT 240
 1 |||G|T|C|E|N|T|R|G|R|N|V|A|V|T|V|S|G|H|T|C|O|H|W|S|A|Q|T|P|H|T|P|R|T|E|N|P|K|C|Q|N|L|D|E|N|Y|C|R|N|P|D|G|K|R|A|P|W|C|T 240

Db 181 GTCENTRGRNVAVTVSGHTCOHWSAQTPHTPRTENPKCQNLDENYCRNPDKRAPWCT 240
 1 |||G|T|C|E|N|T|R|G|R|N|V|A|V|T|V|S|G|H|T|C|O|H|W|S|A|Q|T|P|H|T|P|R|T|E|N|P|K|C|Q|N|L|D|E|N|Y|C|R|N|P|D|G|K|R|A|P|W|C|T 240

QY 241 TNSQVRWECKIPSCDSSPV 260
 1 |||T|N|S|Q|V|R|W|E|C|K|I|P|S|C|D|S|S|P|V 260

Db 241 TNSQVRWECKIPSCDSSPV 260
 1 |||T|N|S|Q|V|R|W|E|C|K|I|P|S|C|D|S|S|P|V 260

RESULT 12

; Sequence 3, Application PC/TUS9505107

PCT-US95-05107-3

GENERAL INFORMATION:

APPLICANT: THE CHILDREN'S MEDICAL CENTER, CORPORATION

TITLE OF INVENTION: Angiostatin and Method of Use

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSE: Jones & Askew

STREET: 191 Peachtree Street, 37th Floor

CITY: Atlanta

STATE: Georgia

COUNTRY: U.S.

ZIP: 30303-1769

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/05107

FILING DATE:

CLASSIFICATION:

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 08/248,629

FILING DATE: 26-APR-1994

APPLICATION NUMBER: US 08/326,785

FILING DATE: 20-OCT-1994

ATTORNEY/AGENT INFORMATION:

NAME: Johnson, James D.

REGISTRATION NUMBER: 31,771

REFERENCE/DOCKET NUMBER: 05213-0122

TELECOMMUNICATION INFORMATION:

TELEPHONE: 404-818-3700

TELEFAX: 404-818-3799

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 339 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ORIGINAL SOURCE:

ORGANISM: Homo sapiens

PCT-US95-05107-3

Query Match 99.7%; Score 1535; DB 5; Length 339;
 Best Local Similarity 99.6%; Pred. No. 1.4e-138;
 Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VYLECKTGNKGNYRGMSKTKNGTQCKNSSTSPPHRPRSPATHPEGLBNYCRNPDN 60
 Db 61 DPOGPWCYTDPDKRYDPCDILCEECMHCSGENYDGKISKTMGLESQADSDSPHAH 120
 Qy 1 VYLECKTGNKGNYRGMSKTKNGTQCKNSSTSPPHRPRSPATHPEGLBNYCRNPDN 60
 Db 61 DPOGPWCYTDPDKRYDPCDILCEECMHCSGENYDGKISKTMGLESQADSDSPHAH 120
 Qy 121 GIYPSKPNKLKKYCNCPDRLRPFCFTDPNPKVHLCDIPRCTTPSSGPTVQLK 180
 Db 121 GIYPSKPNKLKKYCNCPDRLRPFCFTDPNPKVHLCDIPRCTTPSSGPTVQLK 180
 Qy 181 GTGENDYRNVAATVSGHTQHNSAQTPHTHERTPENFCKNDENYCRNPDKGRAPWCH 240
 Db 181 GTGENDYRNVAATVSGHTQHNSAQTPHTHERTPENFCKNDENYCRNPDKGRAPWCH 240
 Qy 241 TNSQVRWYCKLPSCDSSPV 260
 Db 241 TNSQVRWYCKLPSCDSSPV 260

RESULT 14

US-09-377-250-2

Sequence 2, Application US/09377250

PATENT NO. 6365364

GENERAL INFORMATION:

APPLICANT: MANN, KENNETH G.

TITLE OF INVENTION: ANGIOGENESIS INHIBITORS AND USERS THEREOF

FILE REFERENCE: 48A09/360

CURRENT APPLICATION NUMBER: US/09/377,250

CURRENT FILING DATE: 1999-08-19

NUMBER OF SEQ ID NOS: 5

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 2

LENGTH: 375

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: angiogenesis inhibitor

FEATURE: MOD RES

LOCATION: (25)

OTHER INFORMATION: Xaa = Gln or Glu

RESULT 13

US-09-377-250-3

; Sequence 3, Application US/09377250

Query Match 99.7%; Score 1535; DB 3; Length 375;

Best Local Similarity 99.6%; Pred. No. 1.6e-18;
 Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Query Match 99.7%; Score 1535; DB 2; Length 378;
 Best Local Similarity 99.6%; Pred. No. 1.6e-138; Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VVLSBCKTGNGKVRGTMISKNGITCQKWSSTSPPHRPRFSPATHSEGLENYCRNDN 60
 Db 2 VVLSBCKTGNGKVRGTMISKNGITCQKWSSTSPPHRPRFSPATHSEGLENYCRNDN 61

Qy 61 DROGPWCYTDPBKRYCDLCEBECMHSGENTDGKTSKTMSCLECAWDSOPHAH 120
 Db 62 DROGPWCYTDPBKRYCDLCEBECMHSGENTDGKTSKTMSCLECAWDSOPHAH 121

Qy 121 GYPSKPNKNUKKNYCRNPRLPCTTDPKWELCDIPRCTTPSSGPTVCLK 180
 Db 122 GYPSKPNKNUKKNYCRNPRLPCTTDPKWELCDIPRCTTPSSGPTVCLK 181

Qy 181 GTGENYRGNAVAVTSGHTCQHMSAQTPHTRTPENFPCKNLDENYCRNDGKRAPWCH 240
 Db 182 GTGENYRGNAVAVTSGHTCQHMSAQTPHTRTPENFPCKNLDENYCRNDGKRAPWCH 241

Qy 241 TNSQVRWEYCKIPSCDSSPV 260
 Db 242 TNSQVRWEYCKIPSCDSSPV 261

RESULT 15
 US-08-612-788-42
 Sequence 42, Application US/08612788
 Patent No. 5837682
 GENERAL INFORMATION:
 APPLICANT: Folkman, M. Judah
 APPLICANT: O'Reilly, Michael
 APPLICANT: Cao, Yihai
 APPLICANT: Sim, B. Kim Lee
 TITLE OF INVENTION: Angiostatin Fragments and Method of Use
 NUMBER OF SEQUENCES: 45
 CORRESPONDENCE ADDRESS:
 ADDRESSEES: Jones & Askew
 STREET: 191 Peachtree Street, 37th Floor
 CITY: Atlanta
 STATE: Georgia
 COUNTRY: U.S.
 ZIP: 30303-1769

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/612,788
 FILING DATE:

CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Warren, William L.
 REGISTRATION NUMBER: 36,714
 REFERENCE/DOCKET NUMBER: 05213-0126
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 404-818-3700
 TELEFAX: 404-818-3799
 INFORMATION FOR SEQ ID NO: 42:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 378 amino acids
 TYPE: amino acid
 STRANDEDNESS: NO
 HYPOTHETICAL: NO
 TOPOLOGY: linear
 MOLECULE TYPE: protein

FRAGMENT TYPE: N-terminal
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 IMMEDIATE SOURCE:
 CLONE: KI-4BKLS

US-08-612-788-42

Search completed: July 27, 2005, 03:31:19
 Job time : 45 secs

Query Match 99.7%; Score 1535; DB 2; Length 378;
 Best Local Similarity 99.6%; Pred. No. 1.6e-138; Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VVLSBCKTGNGKVRGTMISKNGITCQKWSSTSPPHRPRFSPATHSEGLENYCRNDN 60
 Db 6 VVLSBCKTGNGKVRGTMISKNGITCQKWSSTSPPHRPRFSPATHSEGLENYCRNDN 65

Qy 61 DROGPWCYTDPBKRYCDLCEBECMHSGENTDGKTSKTMSCLECAWDSOPHAH 120
 Db 62 DROGPWCYTDPBKRYCDLCEBECMHSGENTDGKTSKTMSCLECAWDSOPHAH 121

Qy 121 GYPSKPNKNUKKNYCRNPRLPCTTDPKWELCDIPRCTTPSSGPTVCLK 180
 Db 122 GYPSKPNKNUKKNYCRNPRLPCTTDPKWELCDIPRCTTPSSGPTVCLK 181

Qy 181 GTGENYRGNAVAVTSGHTCQHMSAQTPHTRTPENFPCKNLDENYCRNDGKRAPWCH 240
 Db 182 GTGENYRGNAVAVTSGHTCQHMSAQTPHTRTPENFPCKNLDENYCRNDGKRAPWCH 241

Qy 241 TNSQVRWEYCKIPSCDSSPV 260
 Db 242 TNSQVRWEYCKIPSCDSSPV 261

Qy 244 TNSQVRWEYCKIPSCDSSPV 264
 Db 245 TNSQVRWEYCKIPSCDSSPV 265

QY 1 VYLEECKINGNGKNGVAVTWSHTCQHSAQTPHTHTPENFPCKLNDENYCRNPDGKISKTMSGLECOAWDSQPHAH 60
 CC 1 VYLEECKINGNGKNGVAVTWSHTCQHSAQTPHTHTPENFPCKLNDENYCRNPDGKISKTMSGLECOAWDSQPHAH 60
 Db 61 DPGGPWCTTYTPEKRYDYCDDILECEBECMHSGENYDGKISKTMSGLECOAWDSQPHAH 120
 CC 61 DPGGPWCTTYTPEKRYDYCDDILECEBECMHSGENYDGKISKTMSGLECOAWDSQPHAH 120
 QY 121 GYIPSKERNKLUKNYCRNPRLERLWCFTDPKGWELCDIPRCTPPSSGTYQCLK 180
 CC 121 GYIPSKERNKLUKNYCRNPRLERLWCFTDPKGWELCDIPRCTPPSSGTYQCLK 180
 Db 121 GYIPSKERNKLUKNYCRNPRLERLWCFTDPKGWELCDIPRCTPPSSGTYQCLK 180
 QY 181 GTGENYRGNVAVTWSHTCQHSAQTPHTHTPENFPCKLNDENYCRNPDGKRAPWCHT 240
 CC 181 GTGENYRGNVAVTWSHTCQHSAQTPHTHTPENFPCKLNDENYCRNPDGKRAPWCHT 240
 Db 241 TNSQVRWEYCKLPSODSPV 260
 QY 241 TNSQVRWEYCKLPSODSPV 260
 Db 241 TNSQVRWEYCKLPSODSPV 260
 RESULT 2
 AAU01209
 ID AAU01209 standard; protein; 260 AA.
 XX
 AC AAU01209;
 DT 26-SEP-2001 (first entry)
 XX
 DE Human Angiostatin (hASv3) protein.
 XX
 KW Human; Angiostatin; recombinant production; cation exchange column;
 KW fermentation; angiogenesis mediated disease; leukaemia; tumour;
 KW rheumatoid arthritis; plaque neovascularisation.
 OS Homo sapiens.
 XX
 PN WO200140260-A2.
 XX
 PD 07-JUN-2001.
 XX
 PF 04-DEC-2000; 2000WO-US032843.
 PR 03-DBC-1999; 99US-0168919P.
 PA (ENTR-) ENTREMED INC.
 XX
 PI Madsen J, Liang H, Sim KL, Zhou X, Chang-Murad A, Boerner RJ;
 PI Bermejo LL, Mistry FR, Schrimsher JL, Shepard SR;
 DR WPI: 2001-408277/43.
 DR N-PSDB; AMS04181.
 XX
 PT Purifying recombinant angiostatin involves applying fermented broth
 PT containing angiostatin to expanded bed cation exchange column, anion
 PT exchange column, hydroxyapatite column, hydrophobic column and a
 PT membrane.
 XX
 PS Example 1; Page 22; 49pp; English.

The present sequence representing Angiostatin protein is given in an invention providing a method for recombinant production, recovery and purification of Angiostatin protein. Purification of recombinant Angiostatin comprises applying crude fermentation broth containing the protein to an expanded bed cation exchange column, eluting it, and applying the eluate to anion exchange column, repeating the process of eluting and applying to hydroxyapatite column, hydrophobic column and membrane, in order, and collecting fluid passing through the membrane. Angiostatin is useful for treating angiogenesis mediated diseases, including solid tumours, leukemia, tumour metastases, benign tumours and rheumatoid arthritis, psoriasis, ocular angiogenic diseases, Oster-Webber syndrome, myocardial angiogenesis, plaque neovascularisation,

CC relangiectasia, haemophilic joints, angiofibroma and wound granulation.
 As a centrifugation technique is not employed in the process, damage to the cells with concomitant release of undesirable biological materials such as cytochromes, pigments, enzymes, chemicals and other undesirable cellular constituents and debris, is prevented. Large scale recovery and purification of proteins is greater than that obtained from prior art methods. Active Angiostatin can be stored in buffers for extended periods of time, in vials or other containers, either in solution which may be liquid or frozen, or lyophilised

Sequence 260 AA;

Query Match 100 %; Score 1540; DB 4; Length 260;
 Best Local Similarity 100 %; Pred. No. 8.7e-91; Mismatches 0; Indels 0; Gaps 0;

Matches 260; Conservative 0, MisMatches 0; Indels 0; Gaps 0;

QY 1 VYLEECKINGNGKNGVAVTWSHTCQHSAQTPHTHTPENFPCKLNDENYCRNPDGKRAPWCHT 240
 CC 1 VYLEECKINGNGKNGVAVTWSHTCQHSAQTPHTHTPENFPCKLNDENYCRNPDGKRAPWCHT 240
 DB 61 DPGGPWCTTYTPEKRYDYCDDILECEBECMHSGENYDGKISKTMSGLECOAWDSQPHAH 120
 CC 61 DPGGPWCTTYTPEKRYDYCDDILECEBECMHSGENYDGKISKTMSGLECOAWDSQPHAH 120
 QY 61 DPGGPWCTTYTPEKRYDYCDDILECEBECMHSGENYDGKISKTMSGLECOAWDSQPHAH 120
 CC 61 DPGGPWCTTYTPEKRYDYCDDILECEBECMHSGENYDGKISKTMSGLECOAWDSQPHAH 120
 DB 61 DPGGPWCTTYTPEKRYDYCDDILECEBECMHSGENYDGKISKTMSGLECOAWDSQPHAH 120
 QY 121 GYIPSKERNKLUKNYCRNPRLERLWCFTDPKGWELCDIPRCTPPSSGTYQCLK 180
 CC 121 GYIPSKERNKLUKNYCRNPRLERLWCFTDPKGWELCDIPRCTPPSSGTYQCLK 180
 DB 121 GYIPSKERNKLUKNYCRNPRLERLWCFTDPKGWELCDIPRCTPPSSGTYQCLK 180
 QY 181 GTGENYRGNVAVTWSHTCQHSAQTPHTHTPENFPCKLNDENYCRNPDGKRAPWCHT 240
 CC 181 GTGENYRGNVAVTWSHTCQHSAQTPHTHTPENFPCKLNDENYCRNPDGKRAPWCHT 240
 DB 181 GTGENYRGNVAVTWSHTCQHSAQTPHTHTPENFPCKLNDENYCRNPDGKRAPWCHT 240
 QY 241 TNSQVRWEYCKLPSODSPV 260
 CC 241 TNSQVRWEYCKLPSODSPV 260
 DB 241 TNSQVRWEYCKLPSODSPV 260
 RESULT 3
 ADK40316
 ID ADK40316 standard; protein; 869 AA.
 XX
 AC ADK40316;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DS C-terminal albumin-angiostatin fusion protein.
 XX
 PA cytostatic; vaccine; albumin fusion protein; angiogenesis inhibiting peptide; angiogenesis-dependent tumor; cancer; collagen.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO2003066085-A1.
 XX
 PD 14-AUG-2003.
 XX
 PF 07-FEB-2003; 2003WO-1B000433.
 XX
 PR 07-FEB-2002; 2002US-0355547P.
 XX
 PA (AVET) AVENTIS BEHRING GMBH.
 PA (DELB) DELTA BIOTECHNOLOGY LTD.
 XX
 PI Martins P, Celik I, Kisker O, Sleep D, Hay J, Hauser H;
 XX
 DR WPI; 2003-731479/69.
 DR N-PSDB; ADK40315.
 XX
 PT New albumin fusion protein comprising an angiogenesis inhibiting peptide and an albumin having an albumin activity, or their fragments or variants, useful for treating angiogenesis-dependent tumor, e.g. cancer.

XX
PS Disclosure; Fig 8; 136pp; English.

XX
CC The invention relates to an albumin fusion protein comprising an
CC angiogenesis inhibiting peptide and an albumin having an albumin
compositions, vaccines and methods are useful for treating angiogenesis-
CC dependent tumor, e.g. cancer. This sequence represents an C-terminal-
CC albumin-angiostatin fusion protein.

XX
SQ Sequence 869 AA;

Query Match 99.8%; Score 1537; DB 7; Length 869;
Best Local Similarity 99.6%; Pred. No. 4.2e-90; Matches 259; Conservative 1; Mismatches 0; Indels 0; Gaps 0; CQY 1 VVLSBCKTGKNGKNGTMSKTKGNTCKQWSSTSPPHRPRSPATHPSBGLEENYCRNPDN 60
Db 610 VVLSBCKTGKNGKNGTMSKTKGNTCKQWSSTSPPHRPRSPATHPSBGLEENYCRNPDN 669
CQY 61 DROGPWCYTDPERKYDYLSCREBECMGSGENYDKISKMSKGLEQAWDSQPHAH 120
Db 670 DROGPWCYTDPERKYDYLSCREBECMGSGENYDKISKMSKGLEQAWDSQPHAH 729
CQY 121 GYIPSKPKPNKLKKNYCRRNPKRDLRPWCFPTDPNKRWECLDIPRCTTPPSGGTYQCLK 180
Db 730 GYIPSKPKPNKLKKNYCRRNPKRDLRPWCFPTDPNKRWECLDIPRCTTPPSGGTYQCLK 789
CQY 181 GTGENYRGNVAVTVSGHTCOHWSAQOPTPHTHERPENFPCKKLNDENYCRNPDGKRAPWHT 240
Db 790 GTGENYRGNVAVTVSGHTCOHWSAQOPTPHTHERPENFPCKKLNDENYCRNPDGKRAPWHT 849
CQY 241 TNSQVRWEYCKIPSCDSPPV 260
Db 850 TNSQVRWEYCKIPSCDSPPV 869

RESULT 4

ID ADK40314 standard; protein; 869 AA.
XX AC ADK40314;

XX DT 06-MAY-2004 (first entry)

DE N-terminal angiostatin-albumin fusion protein.

XX KW cytostatic; vaccine; albumin fusion protein; angiogenesis-inhibiting peptide; angiogenesis-dependent tumor; cancer; collagen.

XX OS Homo sapiens.
OS Synthetic.

PN WO2003066085-A1.
XX PD 14-AUG-2003.

XX PF 07-FEB-2003; 2003WO-IB000433.

XX PR 07-FEB-2002; 2002US-0355547P.

XX PA (AVETIS) AVENTIS BEHRING GMBH.
PA (DELB) DELTA BIOTECHNOLOGY LTD.

XX PI Mertins P, Celik I, Kisker O, Sleep D, Hay J, Hauser H;
XX DR WPI; 2003-731479/69.

XX DR N-PSDB; ADK40313.

CC New albumin fusion protein comprising an angiogenesis inhibiting peptide
PT and an albumin having an albumin having an albumin activity, or their fragments or
variants, useful for treating angiogenesis-dependent tumor, e.g. cancer.

XX
PS Disclosure; Fig 6; 136pp; English.

XX
CC The invention relates to an albumin fusion protein comprising an
CC angiogenesis inhibiting peptide and an albumin having an albumin
compositions, vaccines and methods are useful for treating angiogenesis-
CC dependent tumor, e.g. cancer. This sequence represents an N-terminal-
CC angiostatin-albumin fusion protein.

XX
SQ Sequence 869 AA;

Query Match 99.8%; Score 1537; DB 7; Length 869;
Best Local Similarity 99.6%; Pred. No. 4.2e-90; Matches 259; Conservative 1; Mismatches 0; Indels 0; Gaps 0; CQY 1 VVLSBCKTGKNGKNGTMSKTKGNTCKQWSSTSPPHRPRSPATHPSBGLEENYCRNPDN 60
Db 25 VVLSBCKTGKNGKNGTMSKTKGNTCKQWSSTSPPHRPRSPATHPSBGLEENYCRNPDN 84
CQY 61 DROGPWCYTDPERKYDYLSCREBECMGSGENYDKISKMSKGLEQAWDSQPHAH 120
Db 85 DROGPWCYTDPERKYDYLSCREBECMGSGENYDKISKMSKGLEQAWDSQPHAH 144
CQY 121 GYIPSKPKPNKLKKNYCRRNPKRDLRPWCFPTDPNKRWECLDIPRCTTPPSGGTYQCLK 180
Db 145 GYIPSKPKPNKLKKNYCRRNPKRDLRPWCFPTDPNKRWECLDIPRCTTPPSGGTYQCLK 204
CQY 181 GTGENYRGNVAVTVSGHTCOHWSAQOPTPHTHERPENFPCKKLNDENYCRNPDGKRAPWHT 240
Db 205 GTGENYRGNVAVTVSGHTCOHWSAQOPTPHTHERPENFPCKKLNDENYCRNPDGKRAPWHT 264
CQY 241 TNSQVRWEYCKIPSCDSPPV 260
Db 265 TNSQVRWEYCKIPSCDSPPV 284

RESULT 5

ID AAG79748 standard; protein; 260 AA.
XX AC AAG79748;

XX DT 18-MAR-2003 (first entry)

DE Human plasminogen kringle domains 1-3, KL-3.

XX KW Human; Plasminogen; angiostatin; neovascularisation; kringle domain; cell proliferation; viral vector; replication-defective; cancer; tumour.

XX OS Homo sapiens.
OS Synthetic.

PN WO200288173-A2.

XX PD 07-NOV-2002.

XX PF 29-APR-2002; 2002WO-US013461.

XX PR 30-APR-2001; 2001US-0287573P.
PR 05-APR-2002; 2002US-0370634P.

XX PA (CELL-) CELL GENESYS INC.

XX PI Chang B, Wu WW, Macarthur J, Patel S, Jooss K, Mendez M;
XX DR WPI; 2003-1913112.

XX DR N-PSDB; ABA00776.

CC New recombinant viral vector expressing human angiostatin useful for
PT inhibiting angiogenesis in a mammalian subject with cancer or tumor.

XX PS Disclosure; Page 75-76; 83pp; English.

XX
PR 01-OCT-1997; 97US-0060609P.
XX
PA (SHAR) SEARLE & CO G D.
XX
PI Bolanowski MA, Caparon MH, Casperson GF, Gregory SA, Klein BK;
PT McKearn JP;
XX DR WPI; 1999-255098/21..
XX PT New multifunctional proteins useful for treating angiogenic-mediated diseases.
XX PS Claim 5; Page 97-98; 121pp; English.

The specification describes multifunctional proteins which comprise combinations of angiostatin, endostatin, intereron, thrombospondin, interferon-inducible protein and platelet factor 4, and have anti-angiogenic and/or anti-tumor activity. The multifunctional protein may exhibit useful properties such as having similar or greater biological activity when compared to a single factor or by having improved half-life or decreased adverse side effects, or a combination of these properties. The proteins can be used for treating an angiogenic-mediated disease, e.g. cancer, diabetic retinopathy, macular degeneration, or arthritis. They can also be used for inhibiting the production of tumor cells (characteristic of lung, breast, ovarian, prostate, gastric, colon, renal, bladder cancers; melanoma, hepatoma, sarcoma and lymphoma) in a patient and for inhibiting tumor growth. The present sequence represents a multifunctional protein of the invention

'SQ Sequence 285 AA;

Query Match Best Local Similarity 99.7%; Score 1535; DB 2; Length 285;

Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 VYLSECKTGNGKNGYRGMSTKNGITCKQWSSSPHRPRSPATHSEGLENYCRNPDN 60
Db 20 VYLSECKTGNGKNGYRGTMSKTKNGITCOKWSSSPHRPRSPATHSEGLENYCRNPDN 79Oy 61 DPOGPWCYTIDPEKRYDYCDILCEBECMHCGENBYRGKISKMSKGLECOAWSOPHAH 120
Db 80 DPOGPWCYTIDPEKRYDYCDILECEBECMHCGENYDKISKTMMSGLECOAWSOPHAH 139Oy 121 GYPSKFPNKLNKKNYCRNPDRLRPPCFTTOPNKRWLCDIPRCPTPPSGPYTQCLK 180
Db 140 GYPSKFPNKLNKKNYCRNPDRLRPPCFTTOPNKRWLCDIPRCPTPPSGPYTQCLK 199Oy 181 GTGENYRGNVAVTWSGHTQHWSAQTPHTHERPENFCKNLBNYCRNPDGKRAPWHT 240
Db 200 GTGENYRGNVAVTWSGHTQHWSAQTPHTHERPENFCKNLBNYCRNPDGKRAPWHT 259Oy 241 TNSQVRWEYCKLIPSCDSSPV 260
Db 260 TNSQVRWEYCKLIPSCDSSPV 279

RESULT 8

AAR83961 ID AAR83961 standard; protein: 339 AA.

XX AC AAR83961;

XX DT 10-MAR-1996 (first entry)
XX Human plaminogen peptide fragment.XX KW Angiotatin; plasminogen; endothelial inhibitor; therapeutic;
XX gene therapy.XX OS Homo sapiens.
XX PN WO9529242-A1.XX
PR 02-NOV-1995.XX
PA 26-APR-1995; 95WO-US005107.XX
PI 26-APR-1994; 94US-0024629.

XX DR 20-OCT-1994; 94US-00326785.

XX PT (CHIL-) CHILDREN'S MEDICAL CENT.

XX PI O'reilly MS, Folkman MJ, Sim KL, Cao Y;
DR WPI; 1995-382990/49.

XX PT Endothelial inhibitor Angiostatin - useful to treat angiogenic mediated disease esp. angiogenesis and cancer.

XX PS Claim 4; Page 81-82; 108pp; English.

The sequence represents a plasminogen fragment which is compared with the corresponding plasminogen fragments of monkey (AAR83962), pig (AAR83963) and cattle (AAR83964) origin (in FIG. 2), as well as the with the first 339 amino acids of mouse angiostatin (AAR83960) (i.e. aa's 98-436 of the complete 812 aa plasminogen molecule AAR83959). Human angiostatin is a plasminogen fragment starting at aa 97 or 99 of the complete plasminogen molecule. Angiostatin is an endothelial inhibitor, which reversibly inhibits proliferation of endothelial cells and thereby inhibits angiogenesis. It is useful in the treatment of a human or animal with diabetic mediated disease e.g. arthritis, macular degeneration, diabetic retinopathy or cancer. Cells comprising angiostatin-coding sequences are useful for gene therapy of primary tumors

XX SQ Sequence 339 AA;

Query Match Best Local Similarity 99.7%; Score 1535; DB 2; Length 339;

Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 VYLSECKTGNGKNGYRGMSTKNGITCKQWSSSPHRPRSPATHSEGLENYCRNPDN 60
Db 61 DPOGPWCYTIDPEKRYDYCDILECEBECMHCGENYDKISKTMMSGLECOAWSOPHAH 120Oy 61 DPOGPWCYTIDPEKRYDYCDILECEBECMHCGENYDKISKTMMSGLECOAWSOPHAH 120
Db 61 DPOGPWCYTIDPEKRYDYCDILECEBECMHCGENYDKISKTMMSGLECOAWSOPHAH 120Oy 121 GYPSKFPNKLNKKNYCRNPDRLRPPCFTTOPNKRWLCDIPRCPTPPSGPYTQCLK 180
Db 121 GYPSKFPNKLNKKNYCRNPDRLRPPCFTTOPNKRWLCDIRCTTPSSGPTYQCLK 180Oy 181 GTGENYRGNVAVTWSGHTQHWSAQTPHTHERPENFCKNLBNYCRNPDGKRAPWHT 240
Db 181 GTGENYRGNVAVTWSGHTQHWSAQTPHTHERPENFCKNLBNYCRNPDGKRAPWHT 240Oy 241 TNSQVRWEYCKLIPSCDSSPV 260
Db 241 TNSQVRWEYCKLIPSCDSSPV 260RESULT 9
AAW07581 ID AAW07581 standard; protein: 339 AA.

XX AC AAW07581;

XX DT 24-JUN-1997 (first entry)
XX DE N-Terminal angiostatin fragment.XX KW angiostatin; plasminogen; kringle; angiogenesis; cancer; arthritis;
XX macular degeneration; diabetic retinopathy.

XX OS Homo sapiens.

XX
PN WO935774-A2.
XX DE.
PD Human angiotatin fragment.
XX 14-NOV-1996.
XX Plasminogen; kingle; endothelial; angiogenesis; tumour; leukaemia;
KW rheumatoid arthritis; psoriasis; ocular angiogenic disease; ulcer;
KW gene therapy; birth control; Crohn's disease; angiotatin.
XX OS Homo sapiens.
XX PH Key Peptide Location/Qualifiers
PT /note= "Kringle 1-3"
PT 6. .255
PT /note= "Kringle 1-2"
PT 6. .84
PT /note= "Kringle 1"
PT 88. .255
PT /note= "Kringle 2-3"
PT 88. .165
PT 178. .255
PT /note= "Kringle 3"
XX BN WO9854217-A1.
XX PD 03-DEC-1998.
XX PR 29-MAY-1998; 98WO-US010979.
XX PR 30-MAY-1997; 97US-0086735.
XX PA (CHIL-) CHILDRENS MEDICAL CENT.
XX PI Folkman MJ, O'reilly MS;
XX DR WPI; 1999-059809/05.
XX PT Use of plasminogen fragments - having an amino acid sequence similar to
PT the kingle 1-5 region, for inhibiting endothelial cell proliferation and
PT angiogenesis.
XX SQ Example 27; Fig 2A-C; 165PP; English.

Query Match 99.7%; Score 1535; DB 2; Length 339;
Best Local Similarity 99.6%; Pred. No. 2.3e-90;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CC That comprises administering to an endothelial cell a plasminogen
CC fragment having an amino acid sequence similar to the kingle 1-5 region
CC of a plasminogen molecule. The plasminogen fragments can be derived from
CC murine, human, Rhesus, porcine or bovine plasminogens. The plasminogen
CC fragments can be used for modulating angiogenesis and treating angiogenic
CC -mediated disease e.g. solid tumours; for treating excessive or abnormal
CC stimulation of endothelial cells; as a birth control agent; and in the
CC treatment of diseases that have angiogenesis as a pathological
CC consequence (see AAW94036 for details on the various diseases the
CC plasminogen fragments can be used to treat). The nucleotide sequences
CC encoding the plasminogen fragments can also be used for gene therapy. The
CC products can be used for the production of antibodies and in detection
CC and diagnosis. Sequences AAW94037 to WO041 represent angiotatin
CC fragments (protein derivatives of angiotatin or plasminogen, having an
CC endothelial cell proliferation activity) of murine, human, Rhesus,
CC porcine and bovine angiotatins respectively. The kingle regions that
CC can be used in the invention are indicated in the features
XX Sequence 339 AA;

CC Query Match 99.7%; Score 1535; DB 2; Length 339;
CC Best Local Similarity 99.6%; Pred. No. 2.3e-90;
CC Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VYLSECKTGKNGNYRGTMKNGITCQKMSSTSPhRPRSPATHPSEGLEENYCRNPDN 60
Db 1 VYLSECKTGKNGNYRGTMKNGITCQKMSSTSPhRPRSPATHPSEGLEENYCRNPDN 60
Qy 61 DROGPWCYTDPEKRYDYCDILECEEECHMCSGENYDGKISKTMGSLCQAWDSQPHAH 120
Db 61 DROGPWCYTDPEKRYDYCDILECEEECHMCSGENYDGKISKTMGSLCQAWDSQPHAH 120
Qy 121 GYIPSKPKPNKLKKGNYCRNPDRERLPRWCFTTDNPKRWELCDIRCTTPPSGPTYCQLK 180
Db 121 GYIPSKPKPNKLKKGNYCRNPDRERLPRWCFTTDNPKRWELCDIRCTTPPSGPTYCQLK 180
Qy 181 GTGCGNYGRGVAATVSGHTCQHNSAQTPHETRIPENFCKPKLNLDENYCRNPDKRAPWHT 240
Db 181 GTGCGNYGRGVAATVSGHTCQHNSAQTPHETRIPENFCKPKLNLDENYCRNPDKRAPWHT 240
Qy 241 TNSQVRWEYCKIPSCDSFV 260
Db 241 TNSQVRWEYCKIPSCDSFV 260
Qy 241 TNSQVRWEYCKIPSCDSFV 260
Db 241 TNSQVRWEYCKIPSCDSFV 260

RESULT 10
AAW94038 ID AAW94038 Standard; protein; 339 AA.
XX AC AAW94038;
XX DT 06-APR-1999 (first entry)

Db 61 DPOCPWCYTDPEKRYDPCDILCEECBMCQANDSQPHAH 120
 Qy 121 GYPSKFENKNUKGNYCNPDRRLPWFCTDPNKRBLCDIPRCTTPSSGGPTVQCLK 180
 Db 121 GYPSKFENKNUKGNYCNPDRRLPWFCTDPNKRBLCDIPRCTTPSSGGPTVQCLK 180
 Qy 181 GTGENYRGNAVTIVSGHTCQHSAQTPTHTPFPCKNDENCRNPDKRAPWCHT 240
 Db 181 GTGENYRGNAVTIVSGHTCQHSAQTPTHTPFPCKNDENCRNPDKRAPWCHT 240
 Qy 241 TNSQVRWYCKIPSCDSSPV 260
 Db 241 TNSQVRWYCKIPSCDSSPV 260

RESULT 11
 AAM5018
 ID AAM5018 standard; protein; 339 AA.
 AC AAM5018;
 XX 12-MAR-2002 (first entry)
 DT DE Human angiotatin.
 KW Angiotatin; plasminogen; human; angiogenesis; endothelial cell; cell proliferation; inhibitor; tumor; antipsoriatic; cytosolic; vasoconstrictive; antitumour; dermatological; antiinflammatory; antidiabetic; antiheuric; antiarthritic; ophthalmological; vulnerary; antiulcer; antibacterial; antiatherosclerotic; gynaecological; antipyretic; cardiant; contraceptive; therapy.

XX OS Homo sapiens.

XX PH . Key Location/Qualifiers
 PT . Region 6. 255 /label= Kringle-1-3
 PT . Region 6. 165 /label= Kringle-1-2
 PT . Region 6. 84 /label= Kringle-1
 PT . Region 88. 255 /label= Kringle-2-3
 PT . Region 88. 165 /label= Kringle-2
 PT . Region 178. 255 /label= Kringle-3

XX US2001029246-A1.
 PN PR 30-MAY-1997; 97US-00866735.
 PR 24-APR-1998; 98US-00066028.
 PR 11-MAY-1999; 99US-00308821.
 PR 22-JUN-1999; 99US-00338387.
 PA (OREI/) O'REILLY M. S.
 PA (FOIK/) FOLKMAN M. J.
 PA (CAOY/) CAO Y.
 PI O'reilly MS, Folkman MJ, Cao Y;
 DR WPI, 2001-64790/74.

XX Inhibiting endothelial cell proliferation, useful for treating angiogenic mediated diseases such as cancer, arthritis, comprises administering plasminogen fragment corresponding to kringle structures of plasminogen molecule.

XX PS Example 27; Fig 2A-C; 70pp; English.
 XX The present sequence is that of human angiotatin. A claimed method of inhibiting endothelial cell proliferation involves administering a plasminogen fragment (PF) having an amino acid sequence similar to the kringle 1-5 region of a plasminogen molecule. This includes a protein, termed angiotatin, defined by its ability to overcome the angiogenic activity of endogenous growth factors and by its amino acid sequence homology and structural similarity to an internal portion of plasminogen, beginning at approximately amino acid 98. The PF is preferably derived from mouse, human, Rhesus monkey, pig or cattle (see AAM5016-21). It is used in methods and compositions for the treatment of an angiogenic-mediated disease, including haemangioma, solid tumours, blood-borne tumours, leukaemia, metastasis, telangiectasia, psoriasis, angiogenesis, Crohn's disease, plaque neovascularisation, coronary collaterals, cerebral collaterals, arteriovenous malformations, ischaemic limb angiogenesis, corneal diseases, rubesis, neovascular glaucoma, diabetic retinopathy, corneal graft rejection, retroviral fibroplasia, haemophilic joints, rheumatoid arthritis, diabetic neovascularisation, Osler-Weber syndrome, macular degeneration, wound healing, peptic ulcer, Helicobacter pylori related diseases, fractures, keloids, vasculogenesis, haemopoiesis, ovulation, menstruation, Placenta, haemorrhage, fever. Angiotatin is also useful as a birth control agent by preventing vascularisation required for embryo implantation. The compositions are particularly useful for treating or repressing the growth of tumours. Administration of angiotatin to a human or animal with prevascularised tumours. Gene therapy methods are also included in the invention.

XX SQ Sequence 339 AA;

Query	Match	99.7%	Score	1535;	DB	4;	Length	339;
Best	Local	Similarity		Pred.	No.	2..3..90-	Indels	0;
Matches		99.6%			0;		Mismatches	1;
							Indels	0;
							Gaps	0;
Qy 1	VYSEBECKTGKNGYRGTMKTKGTCWKSSTSPHRFSPATHRSBGLEENYCRNPDN	60						
Db 1	VYSEBECKTGKNGYRGTMKTKGTCWKSSTSPHRFSPATHRSBGLEENYCRNPDN	60						
Qy 61	DPOCPWCYTDPEKRYDPCDILCEECBMCQANDSQPHAH 120							
Db 61	DPOCPWCYTDPEKRYDPCDILCEECBMCQANDSQPHAH 120							
Qy 121	GYPSKFENKNUKGNYCNPDRRLPWFCTDPNKRBLCDIPRCTTPSSGGPTVQCLK 180							
Db 121	GYPSKFENKNUKGNYCNPDRRLPWFCTDPNKRBLCDIPRCTTPSSGGPTVQCLK 180							
Qy 181	GTGENYRGNAVTIVSGHTCQHSAQTPTHTPFPCKNDENCRNPDKRAPWCHT 240							
Db 181	GTGENYRGNAVTIVSGHTCQHSAQTPTHTPFPCKNDENCRNPDKRAPWCHT 240							
Qy 241	TNSQVRWYCKIPSCDSSPV 260							
Db 241	TNSQVRWYCKIPSCDSSPV 260							

RESULT 12
 ADG47024
 ID ADG47024 standard; protein; 339 AA.
 AC ADG47024;
 XX DT 11-MAR-2004 (first entry)
 XX DE Human angiotatin protein.

XX KW Angiotatin; cell proliferation; angiogenic-mediated disease; cancer; arthritis; macular degeneration; diabetic retinopathy; psoriasis; scleroderma; Crohn's disease; wounds; peptic ulcer; fracture; gene therapy; plasminogen; cyrostatic; ophthalmological; dermatological; antiinflammatory; vulnerary; human.

OS Homo sapiens.
 XX
 PN US2003064926-A1.
 XX
 PD 03-APR-2003.
 XX
 PP 22-APR-2002; 2002US-00127066.
 XX
 PR 26-APR-1994; 94US-00248629.
 PR 20-OCT-1994; 94US-00326785.
 PR 26-APR-1995; 95US-00429743.
 PR 08-MAR-1995; 96US-00612788.
 PR 30-MAY-1997; 97US-00866735.
 PR 24-APR-1998; 98US-00066028.
 PR 11-MAY-1999; 99US-00309821.
 PR 17-JUN-1999; 99US-00335325.
 PR 16-FEB-2001; 2001US-00788142.
 XX
 PA (FOLK/) FOLKMAN M J.
 PA (OREI/) O'REILLY M S.
 PA (CAOY/) CAO Y.
 PA (SIMK/) SIM K L.
 XX
 PI Folkman MJ, O'reilly MS, Cao Y, Sim KL;
 XX
 DR WPI; 2003-540796/51.
 XX
 PT Inhibiting endothelial cell proliferation, useful for treating cancer, arthritis or diabetic retinopathy, comprises administering to an endothelial cell a proliferation-inhibiting amount of an angiotatin fragment.
 PT
 PT Example 27; SEQ ID NO 3; 96pp; English.
 CC
 CC The present invention relates to endothelial inhibitors called angiotatin which reversibly inhibit proliferation of endothelial cells. The invention is useful for diagnosing and treating angiogenesis-mediated diseases such as cancer, arthritis, macular degeneration, diabetic retinopathy, psoriasis, scleroderma, Crohn's disease, wounds, peptic ulcer and fractures. The invention is also useful in gene therapy. The present sequence is the human angiotatin protein.
 XX
 SQ Sequence 339 AA;

```

Query Match 99.7%; Score 1535; DB 7; Length 339;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 VYLSECKTGNGKNYRGTMKNGITCOKWSSTSPHRPRSPATHPSEGLENVCRNPDN 60
Db 1 VYLSECKTGNGKNYRGTMKNGITCOKWSSTSPHRPRSPATHPSEGLENVCRNPDN 60
Qy 61 DPOGWCYTDPKEKYDYCILECEBECMHSGENYDGKISKTSGLCQAWDSQPHAH 120
Db 61 DPQGPWCYTDPKEKYDYCILECEBECMHSGENYDGKISKTSGLCQAWDSQPHAH 120
Qy 121 GYIPSKFPNKGKKQYCRNPDRELPRWCFTDPNKRWELCDIPRCTTPPPSGPYQCK 180
Db 121 GYIPSKFPNKGKKQYCRNPDRELPRWCFTDPNKRWELCDIPRCTTPPPSGPYQCK 180
Qy 181 GTGENDYGRNVTAVTSGHTCOWSACTPHTERTPENPKNLDENYCRNPDGKRAPWCHT 240
Db 181 GTGENDYGRNVTAVTSGHTCOWSACTPHTERTPENPKNLDENYCRNPDGKRAPWCHT 240
Qy 241 TNSQTRWECKXKIPSDSSPV 260
Db 241 TNSQTRWECKXKIPSDSSPV 260
  
```

OS Homo sapiens.
 XX
 AC ADM11543;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Human Plasminogen fragment (angiotatin).
 XX
 KW endothelial cell proliferation; plasminogen; kringle 1-5; angiogenic-mediated disease; cancer; rheumatoid arthritis; psoriasis; diabetic retinopathy; macular degeneration; corneal graft rejection; neovascular glaucoma; retrobulbar fibroplasia; rubesis; Osler-Webber syndrome; myocardial angiogenesis; murine; human; Rhesus; porcine; bovine; angiotatin.
 XX
 OS Homo sapiens.
 XX
 PN US2004023877-A1.
 XX
 DD 05-FEB-2004.
 XX
 PR 27-MAR-2003; 2003US-00401108.
 XX
 PR 26-APR-1994; 94US-00248629.
 PR 20-OCT-1994; 94US-00326785.
 PR 26-APR-1995; 95US-00429743.
 PR 08-MAR-1996; 96US-00612788.
 PR 30-MAY-1997; 97US-00866735.
 PR 12-DEC-1997; 97US-00989477.
 PR 24-APR-1998; 98US-00066028.
 PR 11-MAY-1999; 99US-0030821.
 PR 22-JUN-1999; 99US-0033817.
 PR 16-FEB-2001; 2001US-00788142.
 XX
 PA (OREI/) O'REILLY M S.
 PA (FOLK/) FOLKMAN M J.
 PA (CAOY/) CAO Y.
 XX
 PI O'reilly MS, Folkman MJ, Cao Y;
 XX
 DR WPI; 2004-142673/14.
 XX
 PT New composition comprising an isolated nucleotide sequence that codes for a plasminogen fragment, useful for treating angiogenesis-dependent diseases including cancer, rheumatoid arthritis, psoriasis or macular degeneration.
 XX
 PS Example 18; SEQ ID NO 3; 78pp; English.
 XX
 CC The invention relates to a method of inhibiting endothelial cell proliferation, comprising administering to an endothelial cell a plasminogen fragment having an amino acid sequence similar to that of the kringle 1-5 region of plasminogen. The plasminogen fragment is derived from murine, human, Rhesus, porcine or bovine plasminogen. Also included are the following: (1) a method of treating a mammal with an angiogenesis-mediated disease; (2) a therapeutic composition for inhibiting endothelial cell proliferation comprising a pharmaceutical excipient and the plasminogen fragment; and (3) a method of expressing a plasminogen fragment having an endothelial cell proliferation inhibiting activity. The method is useful for treating angiogenesis-dependent diseases including cancer. Angiogenesis-mediated diseases also include rheumatoid arthritis, psoriasis, diabetic retinopathy, macular degeneration, corneal graft rejection, neovascular glaucoma, retrobulbar fibroplasia, rubesis, Osler-Webber syndrome or myocardial angiogenesis. The present sequence represents human plasminogen fragment (angiotatin).
 XX
 SQ Sequence 339 AA;

```

Query Match 99.7%; Score 1535; DB 8; Length 339;
Best Local Similarity 99.6%; Pred. No. 2.3e-90; Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 VYLSECKTGNGKNYRGTMKNGITCOKWSSTSPHRPRSPATHPSEGLENVCRNPDN 60
  
```

RESULT 13
 ADMIN1543
 ID ADMIN1543 Standard; protein; 339 AA.

Db 1 VYLSECKTGNGKQYRGTMSTKGITCOKWSSSPHRPRSPATHPSBGLEENYCRNPDN 60
 Qy 61 DPGPWCYTDPERKYDPCILECEECMHCSGENYQKISKIMSGLECOAWDSOPHAR 120
 Db 61 DPGPWCYTDPERKYDPCILECEECMHCSGENYQKISKIMSGLECOAWDSOPHAR 120
 Qy 121 GTIPSKEPNPKNLKKNYCRNPDRLRPWCFITDPRCTTTPPSGGPYOCLK 180
 Db 121 GTIPSKEPNPKNLKKNYCRNPDRLRPWCFITDPRCTTTPPSGGPYOCLK 180
 Qy 181 GTGENYRGNVAVTSGHTQHWAQOPTPHTHERPTENFPCKNIDENYCRNPDGKAPWHT 240
 Db 181 GTGENYRGNVAVTSGHTQHWAQOPTPHTHERPTENFPCKNIDENYCRNPDGKAPWHT 240
 Qy 241 TNSQVRWEYCKIPSCDSPV 260
 Db 241 TNSQVRWEYCKIPSCDSPV 260

RESULT 14
 AAY70255 standard; protein: 363 AA.
 XX
 AC AAY70255;
 XX
 DT 06-JUN-2000 (first entry)
 DE Human angiogenesis inhibitor, angiostatin.
 XX
 KW Human; immunoglobulin gamma Fc fragment; angiostatin; immunofusin; angiogenesis; inhibitor; cytosatic; antirheumatoic; antiarrhythmic; antiparotic; antidiabetic; ophthalmological; immunosuppressant; vasotropic; vulnerability; treatment; antiarteriosclerosis; tumour; metastasis; atherosclerosis; psoriasis; rheumatoid arthritis; ocular angiogenic disease; diabetic retinopathy; macular degeneration; myocardial angiogenesis; plaque neovascularization; telangiectasia; wound granulation; keloid scar; gene therapy.
 OS Homo sapiens.
 XX
 PN WO200011033-A2.
 XX
 PD 02-MAR-2000.
 XX
 PR 25-AUG-1999; 99WO-US019329.
 XX
 PA (LEXI-) LEXINGEN PHARM CORP.
 XX
 PI Lo K., Li Y., Gillies SD;
 XX
 DR WPI; 2000-237616/20.
 DR N-PSDB; A4251295.
 XX
 PT Novel fusion protein of angiostatin or endostatin and an immunoglobulin FC region, useful for treating conditions mediated by angiogenesis, such as rheumatoid arthritis, tumors and macular degeneration.
 XX
 PS Example 4; Page 45-46; 68pp; English.

The patent discloses a DNA molecule encoding a fusion protein comprising a signal sequence, an immunoglobulin Fc region, and an angiogenesis inhibitor selected from angiostatin, endostatin, a plaminogen fragment having angiostatin activity, a collagen XVIII fragment having endostatin activity, or combinations of them. The fusion protein (immunofusin) is used to inhibit angiogenesis and to treat diseases or conditions mediated by angiogenesis. Conditions that may be treated include solid tumours, blood born tumours, tumour metastasis, benign tumours including haemangiomas, acoustic neuromas, neurofibromas, trachomas and pyrogenic granulomas, rheumatoid arthritis, psoriasis, ocular angiogenic diseases e.g. diabetic retinopathy, neuropathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retroental fibroplasia, rubesis and Osler-Webber syndrome; myocardial angiogenesis, plaque neovascularisation, telangiectasia, haemophilic joints, angiofibroma, wound granulation, and excessive or abnormal stimulation of endothelial cells, intestinal cells, atherosclerosis, scleroderma and hypertrophic scars i.e. keloid scars. The DNA constructs may be used in gene therapy. The present sequence is a human angiostatin used in the construction of immunofusin containing human immunoglobulin gamma (IgG) Fc fragment.

SQ Sequence 363 AA;

Query Match 99.7%; Score 1555; DB 3; Length 363;
 Best Local Similarity 99.6%; Pred. No. 2.5e-90; Indels 0; Gaps 0;
 Matches 259; Conservative 0; Mismatches 1;

RESULT 15
 AAY02106 standard; protein: 364 AA.
 ID AAY02106
 XX
 AC AAY02106;
 XX
 DT 16-JUL-1999 (first entry)
 DE A multifunctional protein of the invention.
 KW Angiostatin; endostatin; interferon; thrombospondin; interferon-inducible protein; platelet factor 4; anti-angiogenic; anti-tumor; multi-functional protein; angiogenic-mediated disease; cancer; diabetic retinopathy; macular degeneration; arthritis; tumor cell production.
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO916819-A1.
 XX
 PD 08-APR-1999.
 XX
 PF 30-SEP-1998; 98WO-US020464.
 XX
 PR 01-OCT-1997; 97US-0060609P.
 XX
 PA (SEAR) SEARLE & CO G D.
 XX
 PI Bolanowski MA, Caparon MH, Casperson GF, Gregory SA, Klein BK; McKearn JP;
 XX
 DR WPI; 1999-255098/21.
 XX
 PT New multifunctional proteins useful for treating angiogenic-mediated diseases.

PS Claim 5; Page 101-102; 121pp; English.

XX

CC

CC

CC

CC

CC

The specification describes multifunctional proteins which comprise combinations of angiostatin, endostatin, interferon, thrombospondin, interferon-inducible protein and platelet factor 4, and have anti-angiogenic and/or anti-tumor activity. The multifunctional protein may exhibit useful properties such as having similar or greater biological activity when compared to a single factor or by having improved half-life or decreased adverse side effects, or a combination of these properties. The proteins can be used for treating an angiogenesis-mediated disease, e.g. cancer, diabetic retinopathy, macular degeneration, or arthritis. They can also be used for inhibiting the production of tumor cells (characteristic of lung, breast, ovarian, prostate, pancreatic, gastric, colon, renal, bladder cancer; melanoma, hepatoma, sarcoma and lymphoma) in a patient and for inhibiting tumor growth. The present sequence represents a multifunctional protein of the invention

XX

SQ Sequence 364 AA;

Query Match 99.7%; Score 1535; DB 2; Length 364;
Best Local Similarity 99.6%; Prev. No. 2.5e-90; Mismatches 1; Indels 0; Gaps 0;

QY	1	VYLSECKTGNGAKNYRGTMISKWKGITCQKMSSTSPPHRPRFSPATHPSEGLENYCRNPDN	60
Db	3	VYLSECKTGNGAKNYRGTMISKWKGITCQKMSSTSPPHRPRFSPATHPSEGLENYCRNPDN	62
QY	61	DPOGPMWCYTIDPERKDYCDILEBEECHMCSGENYDGKISKTMGLCQAMQSOPHAH	120
Db	63	DPOGPMWCYTIDPERKDYCDILEBEECHMCSGENYDGKISKTMGLCQAMQSOPHAH	122
Qy	121	GYIPSKFPNQLKQNYCRPDRRLPWCFTDPNKRWECDIFRCTTPPPSGPTYQCLK	180
Db	123	GYIPSKFPNQLKQNYCRPDRRLPWCFTDPNKRWECDIFRCTTPPSGPTYQCLK	182
QY	181	GIGENYRGNVAVTWSGHTQHWSAQTPHTHERTRBNFPCKNLDNYCRNPDGKRAPWHT	240
Db	183	GIGENYRGNVAVTWSGHTQHWSAQTPHTHRNIPENFPCKNLDNYCRNPDGKRAPWHT	242
QY	241	TNSQVRWECKIPICDSSPV	260
Db	243	TNSQVRWECKIPICDSSPV	262

Search completed: July 27, 2005; 03:29:02
Job time : 75 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 27, 2005, 03:30:16; Search time 157 Seconds

(without alignments)
644.191 Million cell updates/sec

Title: US-09-502-176-2

Perfect score: 1540

Sequence: 1 VYLSECKTGSNGKNTYRGTM SK..... TNSQVRWEYCKIPSCDSSPV 260

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1741741 seqs, 38892284 residues

Total number of hits satisfying chosen parameters: 1741741

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_*

1: /cgm2_6/ptodata/2/pubpa/US07_PUBCOMB.pep:*

2: /cgm2_6/ptodata/2/pubpa/_PCT_NEW_PUB.pep:*

3: /cgm2_6/ptodata/2/pubpa/US06_NEW_PUB.pep:*

4: /cgm2_6/ptodata/2/pubpa/US07_NEW_PUB.pep:*

5: /cgm2_6/ptodata/2/pubpa/US07_PUBCOMB.pep:*

6: /cgm2_6/ptodata/2/pubpa/_PCTUS_PUBCOMB.pep:*

7: /cgm2_6/ptodata/2/pubpa/US08_NEW_PUB.pep:*

8: /cgm2_6/ptodata/2/pubpa/US08_PUBCOMB.pep:*

9: /cgm2_6/ptodata/2/pubpa/US09_PUBCOMB.pep:*

10: /cgm2_6/ptodata/2/pubpa/US09_PUBCOMB.pep:*

11: /cgm2_6/ptodata/2/pubpa/US09_NEW_PUB.pep:*

12: /cgm2_6/ptodata/2/pubpa/US09_PUBCOMB.pep:*

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15: /cgm2_6/ptodata/2/pubpa/US10C_PUBCOMB.pep:*

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18: /cgm2_6/ptodata/2/pubpa/US10F_PUBCOMB.pep:*

19: /cgm2_6/ptodata/2/pubpa/US11A_PUBCOMB.pep:*

20: /cgm2_6/ptodata/2/pubpa/US11A_PUBCOMB.pep:*

21: /cgm2_6/ptodata/2/pubpa/US60_NEW_PUB.pep:*

22: /cgm2_6/ptodata/2/pubpa/_US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1540	100.0	260	US-10-131-241-61
2	1535	99.7	303	US-10-810-262-11
3	1535	99.7	339	9 US-09-788-142-3
4	1535	99.7	339	9 US-09-761-120-3
5	1535	99.7	339	9 US-09-335-325-3
6	1535	99.7	339	14 US-10-131-241-3
7	1535	99.7	339	14 US-10-127-066-3
8	1535	99.7	339	15 US-10-402-364-3
9	1535	99.7	339	15 US-10-401-368-3
10	1535	99.7	363	14 US-10-292-418-11
11	1535	99.7	378	9 US-09-873-676-1

ALIGNMENTS

RESULT 1

; Sequence 61, Application US/10431241

Publication No. US20030012792A1

GENERAL INFORMATION:

APPLICANT: Holaday, John W.

APPLICANT: Fortier, Anne H.

TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Proliferation and Regulating Angiogenesis Using Cancer Markers

FILE REFERENCE: 05213-0344 43170-27165

CURRENT APPLICATION NUMBER: US/10/131-241

CURRENT FILING DATE: 2002-07-22

PRIOR APPLICATION NUMBER: US 09/413, 049

PRIOR FILING DATE: 1999-10-05

PRIOR APPLICATION NUMBER: US 09/316, 802

PRIOR FILING DATE: 1998-05-22

NUMBER OF SEQ ID NOS: 65

SOFTWARE: PatentIn version 3.1

SEQ ID NO 61

LENGTH: 260

TYPE: PTM

ORGANISM: Homo sapiens

US-10-131-241-61

Query Match Similarity 100.0%; Score 1540; DB 14; Length 260;
Best Local Similarity 100.0%; Pred. No. 2a-120;
Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q 1 VYLSECKTGSNGKNTYRGTM SK..... TNSQVRWEYCKIPSCDSSPV 260
D 1 VYLSECKTGSNGKNTYRGTM SK..... TNSQVRWEYCKIPSCDSSPV 260

Qy 61 DPOGPMWCYTDPERKYDYCIDECEBECMCMSGENDYDGKTSKTMGLCQAMQSOPHAN 120
 Db 61 DPOGPMWCYTDPERKYDYCIDECEBECMCMSGENDYDGKTSKTMGLCQAMQSOPHAN 120
 Qy 121 GYISPKFPNKLKKNYCRNPDRRELWPWCFTTDPNKRWECDIPRCTTPSSGPTYOCLK 180
 Db 121 GYISPKFPNKLKKNYCRNPDRRELWPWCFTTDPNKRWECDIPRCTTPSSGPTYOCLK 180
 Qy 181 GTGENYRGNAVTWSGHTCQWSAQTPHTERTPENPCNLDENYCRNPGRAPWCHT 240
 Db 181 GTGENYRGNAVTWSGHTCQWSAQTPHTERTPENPCNLDENYCRNPGRAPWCHT 240
 Qy 241 TNSQVRWECKIPSCDSSPV 260
 Db 241 TNSQVRWECKIPSCDSSPV 260

RESULT 2
 US-10-810-262-11
 ; Sequence 11, Application US/10810262
 ; Publication No. US20040234505A1
 ; GENERAL INFORMATION:
 ; APPLICANT: NAYLOR, STUART
 ; APPLICANT: KINGSMAN, SUSAN MARY
 ; APPLICANT: BINLEY, KATIE
 ; TITLE OF INVENTION: POLYNUCLEOTIDE CONSTRUCTS AND USES THEREOF
 ; FILE REFERENCE: 674323-2029.1
 ; CURRENT APPLICATION NUMBER: US/10/810,262
 ; CURRENT FILING DATE: 2004-03-26
 ; PRIOR APPLICATION NUMBER: 09/787,562
 ; PRIOR FILING DATE: 2001-07-06
 ; PRIOR APPLICATION NUMBER: PCT/GB99/03181
 ; PRIOR FILING DATE: 1999-09-22
 ; PRIOR APPLICATION NUMBER: PCT/GB98/02885
 ; PRIOR FILING DATE: 1998-09-23
 ; PRIOR APPLICATION NUMBER: GB 9901906.9
 ; PRIOR FILING DATE: 1999-01-28
 ; PRIOR APPLICATION NUMBER: GB 9903538.8
 ; PRIOR FILING DATE: 1999-02-16
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn Ver. 3.2
 ; SEQ ID NO: 11
 ; LENGTH: 303
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-810-262-11

Query Match 99.7%; Score 1535; DB 16; Length 303;
 Best Local Similarity 99.6%; Pred. No. 6.1e-120; Indels 0; Gaps 0;
 Matches 259; Conservative 0; Mismatches 1;

Qy 1 VLSRCKTGNGKRGTMKTKNGTCKQMSSTSPPHRPRFSPATHPSGLEENYCRPDN 60
 Db 33 VLSRCKTGNGKRGTMKTKNGTCKQMSSTSPPHRPRFSPATHPSGLEENYCRPDN 92
 Qy 61 DPOGPMWCYTDPERKYDYCIDECEBECMCMSGENDYDGKTSKTMGLCQAMQSOPHAN 120
 Db 93 DPOGPMWCYTDPERKYDYCIDECEBECMCMSGENDYDGKTSKTMGLCQAMQSOPHAN 152
 Qy 121 GYISPKFPNKLKKNYCRNPDRRELWPWCFTTDPNKRWECDIPRCTTPSSGPTYOCLK 180
 Db 153 GYISPKFPNKLKKNYCRNPDRRELWPWCFTTDPNKRWECDIPRCTTPSSGPTYOCLK 212
 Qy 181 GTGENYRGNAVTWSGHTCQWSAQTPHTERTPENPCNLDENYCRNPGRAPWCHT 240
 Db 213 GTGENYRGNAVTWSGHTCQWSAQTPHTERTPENPCNLDENYCRNPGRAPWCHT 272
 Qy 241 TNSQVRWECKIPSCDSSPV 260
 Db 273 TNSQVRWECKIPSCDSSPV 292

US-09-788-142-3
 ; Sequence 3, Application US/09788142
 ; Patent No. US2001029246A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Folkman, M. Judah O'Reilly, Michael
 ; TITLE OF INVENTION: Angiotatin Fragments and Method of Use
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Jones & Askew, LLP
 ; STREET: 191 Peachtree Street, 37th Floor
 ; CITY: Atlanta
 ; STATE: Georgia
 ; COUNTRY: USA
 ; ZIP: 30303-1769
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION NUMBER: US/09/788,142
 ; APPLICATION NUMBER: US/09/787,714
 ; FILING DATE: 16-Feb-2001
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/866,735
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Warren, William L.
 ; REGISTRATION NUMBER: 36-714
 ; REFERENCE/DOCKET NUMBER: 05940-0129
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (404) 818-3700
 ; TELEFAX: (404) 818-3799
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 339 amino acids
 ; TYPE: amino acid
 ; STRANDBNESS: <Unknown>
 ; TOPOLOGI: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE: N-terminal
 ; ORIGINAL SOURCE:
 ; ORGANISM: Homo sapiens
 ; IMMEDIATE SOURCE:
 ; CLONE: Angiotatin fragment
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 ; US-09-788-142-3

Query Match 99.7%; Score 1535; DB 9; Length 339;
 Best Local Similarity 99.6%; Pred. No. 6.9e-120; Indels 0; Gaps 0;
 Matches 259; Conservative 0; Mismatches 1;

Qy 1 VLSRCKTGNGKRGTMKTKNGTCKQMSSTSPPHRPRFSPATHPSGLEENYCRPDN 60
 Db 1 VLSRCKTGNGKRGTMKTKNGTCKQMSSTSPPHRPRFSPATHPSGLEENYCRPDN 60
 Qy 61 DPOGPMWCYTDPERKYDYCIDECEBECMCMSGENDYDGKTSKTMGLCQAMQSOPHAN 120
 Db 61 DPOGPMWCYTDPERKYDYCIDECEBECMCMSGENDYDGKTSKTMGLCQAMQSOPHAN 120
 Qy 121 GYISPKFPNKLKKNYCRNPDRRELWPWCFTTDPNKRWECDIPRCTTPSSGPTYOCLK 180
 Db 153 GYISPKFPNKLKKNYCRNPDRRELWPWCFTTDPNKRWECDIPRCTTPSSGPTYOCLK 212
 Qy 181 GTGENYRGNAVTWSGHTCQWSAQTPHTERTPENPCNLDENYCRNPGRAPWCHT 240
 Db 213 GTGENYRGNAVTWSGHTCQWSAQTPHTERTPENPCNLDENYCRNPGRAPWCHT 272
 Qy 241 TNSQVRWECKIPSCDSSPV 260
 Db 273 TNSQVRWECKIPSCDSSPV 292

Qy 181 GTGENYRGNAVTWSGHTCQWSAQTPHTERTPENPCNLDENYCRNPGRAPWCHT 240
 Db 181 GTGENYRGNAVTWSGHTCQWSAQTPHTERTPENPCNLDENYCRNPGRAPWCHT 240
 Qy 241 TNSQVRWECKIPSCDSSPV 260

Db. 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 4

US-09-761-120-3

; Sequence 3, Application US/09761120

; GENERAL INFORMATION:

APPLICANT: Folkman, M. Judah

APPLICANT: O'Reilly, Michael

TITLE OF INVENTION: Nucleic Acids Encoding Kringle 1-5 Region Fragments of Plasminogen

FILE REFERENCE: 0594-0151 (43177-25208)

CURRENT APPLICATION NUMBER: US/09/761,120

CURRENT FILING DATE: 2001-01-16

PRIOR APPLICATION NUMBER: 09/309,821

PRIOR FILING DATE: 1999-05-11

PRIOR APPLICATION NUMBER: 08/866,735

PRIOR FILING DATE: 1997-05-30

NUMBER OF SEQ ID NOS: 47

SOFTWARE: PatentIn version 3.0

SEQ ID NO 3

LENGTH: 339

TYPE: PRT

ORGANISM: Homo sapiens

Query Match 99.7%; Score 1535; DB 9; Length 339;
Best Local Similarity 99.6%; Pred. No. 6.9e-120;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VVLSCKTGGKNGKVRGTMSTKNGITCOKWSSSPHRPRSPATHSBGLAEVNCRNPDN 60

Db 1 VVLSCKTGGKNGKVRGTMSTKNGITCOKWSSSPHRPRSPATHSEGULBNYCRNPDN 60

Qy 61 DPGQPCWCTTDPEKRYCDLCEBECMHCCGENYDKGKISKMSGLCGOAWDSOPHAH 120

Db 61 DPGQPCWCTTDPEKRYCDLCEBECMHCCGENYDKGKISKMSGLCGOAWDSOPHAH 120

Qy 121 GYIPSKPKPNKLKKYCNCRPDRBLPWCFTTPNPKMLCDIRCTPPSGPTYQCLK 180

Db 121 GYIPSKPKPNKLKKYCNCRPDRBLPWCFTTPNPKMLCDIRCTPPSGPTYQCLK 180

Qy 181 GTGENTRGNVAVTVSGHTCQHWSAQTPHTHERTPENFPCKNLDENTCRNPDKRAPWCHT 240

Db 181 GTGENTRGNVAVTVSGHTCQHWSAQTPHTHERTPENFPCKNLDENTCRNPDKRAPWCHT 240

Qy 241 TNSQVRWEYCKIPSCDSSPV 260

Db 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 5 US-09-335-325-3

; Sequence 3, Application US/09335325

; GENERAL INFORMATION:

APPLICANT: Folkman, M. Judah

APPLICANT: O'Reilly, Michael

APPLICANT: Cao, Yihai

APPLICANT: Sim, B. Kim Lee

TITLE OF INVENTION: Angiotatin Fragments and Method of Use

NUMBER OF SEQUENCES: 45

CORRESPONDENCE ADDRESS:

ADDRESSE: Jones & Askew

STREET: 191 Peachtree Street, 37th Floor

CITY: Atlanta

STATE: Georgia

COUNTRY: U.S.

ZIP: 30303-1769

COMPUTER READABLE FORM:
COMPUTER: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/335,325
FILING DATE: 17-Jun-1999
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/612,788

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Warren, William L.

REGISTRATION NUMBER: 36,714

REFERENCE/DOCKET NUMBER: 05213-0126
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
STRANDBNESS: <Unknown>
TOPOLOGY: Linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: N-terminal

ORIGINAL SOURCE:
ORGANISM: Homo sapiens

IMMEDIATE SOURCE:
CLONE: Angiotatin fragment

SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-09-335-325-3

Query Match 99.7%; Score 1535; DB 9; Length 339;
Best Local Similarity 99.6%; Pred. No. 6.9e-120;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VVLSCKTGGKNGKVRGTMSTKNGITCOKWSSSPHRPRSPATHSBGLAEVNCRNPDN 60

Db 1 VVLSCKTGGKNGKVRGTMSTKNGITCOKWSSSPHRPRSPATHSEGULBNYCRNPDN 60

Qy 61 DPGQPCWCTTDPEKRYCDLCEBECMHCCGENYDKGKISKMSGLCGOAWDSOPHAH 120

Db 61 DPGQPCWCTTDPEKRYCDLCEBECMHCCGENYDKGKISKMSGLCGOAWDSOPHAH 120

Qy 121 GYIPSKPKPNKLKKYCNCRPDRBLPWCFTTPNPKMLCDIRCTPPSGPTYQCLK 180

Db 121 GYIPSKPKPNKLKKYCNCRPDRBLPWCFTTPNPKMLCDIRCTPPSGPTYQCLK 180

Qy 181 GTGENTRGNVAVTVSGHTCQHWSAQTPHTHERTPENFPCKNLDENTCRNPDKRAPWCHT 240

Db 181 GTGENTRGNVAVTVSGHTCQHWSAQTPHTHERTPENFPCKNLDENTCRNPDKRAPWCHT 240

Qy 241 TNSQVRWEYCKIPSCDSSPV 260

Db 241 TNSQVRWEYCKIPSCDSSPV 260

RESULT 6 US-10-131-241-3

; Sequence 3, Application US/10131241

; GENERAL INFORMATION:
Publication No. US20030012792A1

APPLICANT: Holaday, John W.

APPLICANT: Portier, Anne H.

TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Proliferation

FILE REFERENCE: 05213-0344 43170-27155

CURRENT APPLICATION NUMBER: US/10/131,241

CURRENT FILING DATE: 2002-07-22

PRIOR APPLICATION NUMBER: US 09/413,049

PRIOR FILING DATE: 1999-10-05

PRIOR APPLICATION NUMBER: US 09/316,802

PRIOR FILING DATE: 1999-05-21

PRIOR APPLICATION NUMBER: US 60/086,586
 PRIORITY FILING DATE: 1998-05-22
 NUMBER OF SEQ ID NOS: 65
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 3
 LENGTH: 339
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-131-241-3

Query Match 99.7%; Score 1535; DB 14; Length 339;

Best Local Similarity 99.6%; Pred. No. 6.9e-120; Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VVLSCECKTGNGKNGYRGTMNSKTKNGTICRKWWSSTSPHRPRFSPATHSEGLENYCRNPDN 60
 Db 1 VVLSCECKTGNGKNGYRGTMNSKTKNGTICRKWWSSTSPHRPRFSPATHSEGLENYCRNPDN 60

QY 61 DPOGPWCYTDPDKRYDYLCEBECMHSGENYDGKISKTMMSGLEQAWDSQPHAH 120
 Db 61 DPOGPWCYTDPDKRYDYLCEBECMHSGENYDGKISKTMMSGLEQAWDSQPHAH 120

QY 121 GYPSKEPNKNUKKNYCRNPDRBLPWCFTDPNKRMLCDIPRCITPPRSSGPTYQCLK 180
 Db 121 GYPSKEPNKNUKKNYCRNPDRBLPWCFTDPNKRMLCDIPRCITPPRSSGPTYQCLK 180

QY 181 GTGENYRGNVAVTVSGHTCOWSAQTPTHRTPEFPCKLUDENYCRNPDKRAPWCHT 240
 Db 181 GTGENYRGNVAVTVSGHTCOWSAQTPTHRTPEFPCKLUDENYCRNPDKRAPWCHT 240

QY 241 TNSQVRWEYCKIPSCSSPV 260
 Db 241 TNSQVRWEYCKIPSCSSPV 260

RESULT 8
 US-10-402-364-3
 Sequence 3, Application US/10402364
 Publication No. US20040024591
 GENERAL INFORMATION:
 APPLICANT: O'Reilly, Michael
 APPLICANT: Folkman, M. Judah
 TITLE OF INVENTION: Nucleic Acids Encoding Kringle 1-5 Region Fragments of Plasminogen
 FILE REFERENCE: 05213-2151 (43170-25208)
 CURRENT FILING DATE: 2003-03-28
 PRIOR APPLICATION NUMBER: US/09/761,120A
 PRIOR FILING DATE: 2001-01-16
 PRIOR APPLICATION NUMBER: 091309, 821
 PRIOR FILING DATE: 1999-05-11
 PRIOR APPLICATION NUMBER: 081866, 735
 PRIOR FILING DATE: 1997-05-30
 NUMBER OF SEQ ID NOS: 52
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 3
 LENGTH: 339
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-402-364-3

Query Match 99.7%; Score 1535; DB 15; Length 339;

Best Local Similarity 99.6%; Pred. No. 6.9e-120; Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VVLSCECKTGNGKNGYRGTMNSKTKNGTICRKWWSSTSPHRPRFSPATHSEGLENYCRNPDN 60
 Db 1 VVLSCECKTGNGKNGYRGTMNSKTKNGTICRKWWSSTSPHRPRFSPATHSEGLENYCRNPDN 60

QY 61 DPOGPWCYTDPDKRYDYLCEBECMHSGENYDGKISKTMMSGLEQAWDSQPHAH 120
 Db 61 DPOGPWCYTDPDKRYDYLCEBECMHSGENYDGKISKTMMSGLEQAWDSQPHAH 120

QY 121 GYPSKEPNKNUKKNYCRNPDRBLPWCFTDPNKRMLCDIPRCITPPRSSGPTYQCLK 180
 Db 121 GYPSKEPNKNUKKNYCRNPDRBLPWCFTDPNKRMLCDIPRCITPPRSSGPTYQCLK 180

QY 181 GTGENYRGNVAVTVSGHTCOWSAQTPTHRTPEFPCKLUDENYCRNPDKRAPWCHT 240
 Db 181 GTGENYRGNVAVTVSGHTCOWSAQTPTHRTPEFPCKLUDENYCRNPDKRAPWCHT 240

QY 241 TNSQVRWEYCKIPSCSSPV 260
 Db 241 TNSQVRWEYCKIPSCSSPV 260

RESULT 7
 US-10-127-066-3
 Sequence 3, Application US/10127066
 Publication No. US20030064926A1
 GENERAL INFORMATION:
 APPLICANT: O'Reilly, Michael S.
 APPLICANT: Folkman, M. Judah
 APPLICANT: Cao, Yihai
 APPLICANT: Sim, Kim Lee
 TITLE OF INVENTION: Angiotatin Fragments and Method of Use
 FILE REFERENCE: 05213-0612 43170-272529
 CURRENT APPLICATION NUMBER: US/10/127,066
 CURRENT FILING DATE: 2002-07-23
 NUMBER OF SEQ ID NOS: 45
 SEQ ID NO 3
 LENGTH: 339
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-127-066-3

Query Match 99.7%; Score 1535; DB 14; Length 339;

Best Local Similarity 99.6%; Pred. No. 6.9e-120; Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VVLSCECKTGNGKNGYRGTMNSKTKNGTICRKWWSSTSPHRPRFSPATHSEGLENYCRNPDN 60
 Db 1 VVLSCECKTGNGKNGYRGTMNSKTKNGTICRKWWSSTSPHRPRFSPATHSEGLENYCRNPDN 60

QY 61 DPOGPWCYTDPDKRYDYLCEBECMHSGENYDGKISKTMMSGLEQAWDSQPHAH 120
 Db 61 DPOGPWCYTDPDKRYDYLCEBECMHSGENYDGKISKTMMSGLEQAWDSQPHAH 120

QY 121 GYPSKEPNKNUKKNYCRNPDRBLPWCFTDPNKRMLCDIPRCITPPRSSGPTYQCLK 180
 Db 121 GYPSKEPNKNUKKNYCRNPDRBLPWCFTDPNKRMLCDIPRCITPPRSSGPTYQCLK 180

QY 181 GTGENYRGNVAVTVSGHTCOWSAQTPTHRTPEFPCKLUDENYCRNPDKRAPWCHT 240
 Db 181 GTGENYRGNVAVTVSGHTCOWSAQTPTHRTPEFPCKLUDENYCRNPDKRAPWCHT 240

QY 241 TNSQVRWEYCKIPSCSSPV 260
 Db 241 TNSQVRWEYCKIPSCSSPV 260

RESULT 9
 US-10-401-108-3
 Sequence 3, Application US/10401108
 Publication No. US20040023877A1
 GENERAL INFORMATION:
 APPLICANT: Folkman, M. Judah
 APPLICANT: O'Reilly, Michael S.
 TITLE OF INVENTION: Angiotatin Fragments and Method of Use
 NUMBER OF SEQUENCES: 6
 ADDRESSEE: Jones & Askew, LLP
 STREET: 191 Peachtree Street, 37th Floor
 CITY: Atlanta
 STATE: Georgia
 COUNTRY: USA

ZIP: 30303-1769
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 CURRENT APPLICATION DATA: PatentIn Release #1.0, Version #1.30
 APPLICATION NUMBER: US/10/401,108
 FILING DATE: 27-Mar-2003
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/866,735
 FILING DATE: 30-MAY-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Warren, William L.
 REGISTRATION NUMBER: 36,714
 REFERENCE/DOCKET NUMBER: 05940-0129
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (404) 818-3799
 TELEFAX: (404) 818-3799
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 339 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: N-terminal
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 IMMEDIATE SOURCE:
 CLONE: Angiostatin fragment
 SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 US-10-401-108-3

Query Match 99.7%; Score 1535; DB 15; length 339;
 Best Local Similarity 99.6%; Pred. No. 6.9e-120; Indels. 0; Gaps 0;
 Matches 259; Conservative 0; Mismatches 1; Length: 339;

Qy 1 VYLSECKTGNKGNYRGTMSKTKNGITCKQWSSTSPhRRPRSPATHPSGLEENYCRNDN 60
 Db 1 VYLSECKTGNKGNYRGTMSKTKNGITCKQWSSTSPhRRPRSPATHPSGLEENYCRNDN 60
 Qy 2 VYLSECKTGNKGNYRGTMSKTKNGITCKQWSSTSPhRRPRSPATHPSGLEENYCRNDN 61
 Db 2 VYLSECKTGNKGNYRGTMSKTKNGITCKQWSSTSPhRRPRSPATHPSGLEENYCRNDN 61

Qy 61 DPGPWCYTTPBKRVDYCQDLCERECMIGSGENYDGKSKTMGQLEQAWDSQPHAH 120
 Db 62 DPGPWCYTTPBKRVDYCQDLCERECMIGSGENYDGKSKTMGQLEQAWDSQPHAH 121

Qy 121 GYIPSKPNKLNKKNYCRNPDRLRPWCFIDPNKRWELCDIPRCITPPSSGPYQCLK 180
 Db 122 GYIPSKPNKLNKKNYCRNPDRLRPWCFIDPNKRWELCDIPRCITPPSSGPYQCLK 181

Qy 181 GTGENTRGNVAVTVSHTCOIWSACTPHTHERTPENPCKNLDENYCRAPDGKRAPWCHT 240
 Db 182 GTGENTRGNVAVTVSHTCOIWSACTPHTHRTPENPCKNLDENYCRAPDGKRAPWCHT 241

Qy 241 TNSQVRWEYCKIPSCDSSPV 260
 Db 242 TNSQVRWEYCKIPSCDSSPV 261

RESULT 11
 US-09-873-676-1
 Sequence 1, Application US/09873676.
 ; Patent No. US20020077289A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Macdonald, Nicholas J.
 ; TITLE OF INVENTION: Angiostatin and Endostatin Binding Proteins and Methods of Use
 FILE REFERENCE: 052110-0378 (43170-59333)
 CURRENT FILING DATE: 2001-06-04
 PRIOR APPLICATION NUMBER: US 60/209,065
 PRIOR FILING DATE: 2000-06-02
 PRIOR APPLICATION NUMBER: US 60/289,387
 PRIOR FILING DATE: 2001-05-08
 NUMBER OF SEQ ID NOS: 123
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 1
 LENGTH: 378
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-873-676-1

Query Match 99.7%; Score 1335; DB 9; length 378;
 Best Local Similarity 99.6%; Pred. No. 7.8e-120; Indels. 0; Gaps 0;
 Matches 259; Conservative 0; Mismatches 1; Length: 378;

Qy 1 VYLSECKTGNKGNYRGTMSKTKNGITCKQWSSTSPhRRPRSPATHPSGLEENYCRNDN 60
 Db 6 VYLSECKTGNKGNYRGTMSKTKNGITCKQWSSTSPhRRPRSPATHPSGLEENYCRNDN 65

Qy 61 DPGPWCYTTPBKRVDYCQDLCERECMIGSGENYDGKSKTMGQLEQAWDSQPHAH 120
 Db 66 DPGPWCYTTPBKRVDYCQDLCERECMIGSGENYDGKSKTMGQLEQAWDSQPHAH 125

RESULT 12
 US-09-335-325-42
 ; Sequence 42; Application US/09335325
 ; Patent No. US2002016477A1
 GENERAL INFORMATION:
 APPLICANT: Folman, M. Judah
 Cao, Yihai
 Sim, B. Kim Lee
 TITLE OF INVENTION: Angiotatin Fragments and Method of Use
 NUMBER OF SEQUENCES: 45
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Jones & Askew
 STREET: 191 Peachtree Street, 37th Floor
 CITY: Atlanta
 STATE: Georgia
 COUNTRY: U.S.
 ZIP: 30303-1769
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 CURRENT APPLICATION DATA:
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 APPLICATION NUMBER: US/09/335, 325
 FILING DATE: 17-Jun-1999
 CLASSIFICATION: <Unknown>
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/08/612, 788
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Warren, William L.
 REGISTRATION NUMBER: 36,714
 REFERENCE/DOCKET NUMBER: 05213-0126
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 404-818-3700
 TELEFAX: 404-818-3799
 INFORMATION FOR SEQ ID NO: 42:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 378 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: N-terminal
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 IMMEDIATE SOURCE:
 CLONE: KI-4BKLS
 SEQUENCE DESCRIPTION: SEQ ID NO: 42:
 US-09-335-325-42

Query Match, Best Local Similarity 99.7%; Score 1535; DB 14; Length 378;
 Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VYLSECKTNGKRYTMTSKMKGTCQKQSSTSPPRSPATPSEGLENVCRNPDN 60
 Db 6 VYLSECKTNGKRYTMTSKMKGTCQKQSSTSPPRSPATPSEGLENVCRNPDN 65

Qy 61 DRQGPWCYTDPKRYDVCOLCEBECMHCSGENYDGKISKTMGLCQAWDSOPHAH 120
 Db 6 DROGPWCYTDPKRYDVCOLCEBECMHCSGENYDGKISKTMGLCQAWDSOPHAH 125

Qy 121 GYPSKEPNKLKKVCRNPDRPWCFTDPNKRWECLDIPRCITPPSSGPTVCLK 180
 Db 126 GYPSKEPNKLKKVCRNPDRPWCFTDPNKRWECLDIPRCITPPSSGPTVCLK 185

Qy 181 GTGENYRGNAVTAVSGHTCQHSAQTPTHTPENPCPKOLDENYCRNPDGKRAPWCHT 240
 Db 186 GTGENYRGNAVTAVSGHTCQHSAQTPTHTPENPCPKOLDENYCRNPDGKRAPWCHT 245

Qy 241 TNSQVRWEYCKLPSCDSSPV 260
 Db 246 TNSQVRWEYCKLPSCDSSPV 265

RESULT 13
 US-10-131-241-42
 ; Sequence 42; Application US/10131241
 ; Publication No. US20030012792A1
 GENERAL INFORMATION:
 APPLICANT: Holaday, John W.
 TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Proliferation
 FILE REFERENCE: 05213-0344 43170-27156
 CURRENT APPLICATION NUMBER: US/10/131,241
 CURRENT FILING DATE: 2002-07-22
 PRIOR APPLICATION NUMBER: US 09/413, 049
 PRIOR FILING DATE: 1998-10-06
 PRIOR APPLICATION NUMBER: US 09/316, 802
 PRIOR FILING DATE: 1999-05-21
 PRIOR APPLICATION NUMBER: US 60/086, 586
 PRIOR FILING DATE: 1998-05-22
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 42
 LENGTH: 378
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-131-241-42

Query Match, Best Local Similarity 99.7%; Score 1535; DB 14; Length 378;
 Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VYLSECKTNGKRYTMTSKMKGTCQKQSSTSPPRSPATPSEGLENVCRNPDN 60
 Db 6 VYLSECKTNGKRYTMTSKMKGTCQKQSSTSPPRSPATPSEGLENVCRNPDN 65

Qy 61 DRQGPWCYTDPKRYDVCOLCEBECMHCSGENYDGKISKTMGLCQAWDSOPHAH 120
 Db 6 DROGPWCYTDPKRYDVCOLCEBECMHCSGENYDGKISKTMGLCQAWDSOPHAH 125

Qy 121 GYPSKEPNKLKKVCRNPDRPWCFTDPNKRWECLDIPRCITPPSSGPTVCLK 180
 Db 126 GYPSKEPNKLKKVCRNPDRPWCFTDPNKRWECLDIPRCITPPSSGPTVCLK 185

Qy 181 GTGENYRGNAVTAVSGHTCQHSAQTPTHTPENPCPKOLDENYCRNPDGKRAPWCHT 240
 Db 186 GTGENYRGNAVTAVSGHTCQHSAQTPTHTPENPCPKOLDENYCRNPDGKRAPWCHT 245

Qy 241 TNSQVRWEYCKLPSCDSSPV 260
 Db 246 TNSQVRWEYCKLPSCDSSPV 265

RESULT 14
 US-10-127-066-42

Query Match, Best Local Similarity 99.6%; Pred. No. 7.8e-120; Mismatches 1; Indels 0; Caps 0; Matches 259; Conservative 0; Mismatches 1; Indels 0; Caps 0;

1 VYLSECKTNGKRYTMTSKMKGTCQKQSSTSPPRSPATPSEGLENVCRNPDN 60

Sequence 42, Application US/10127066
 Publication No. US2003004926A1
 GENERAL INFORMATION:
 APPLICANT: O'Reilly, Michael S.
 APPLICANT: Folkman, M. Judah
 APPLICANT: Cao, Yihai
 APPLICANT: Sim, Kim Lee
 TITLE OF INVENTION: Angiotatin Fragments and Method of Use
 FILE REFERENCE: 05213-0612 43170-727529
 CURRENT APPLICATION NUMBER: US/10/127.066
 CURRENT FILING DATE: 2002-07-23
 NUMBER OF SEQ ID NOS: 45
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 42
 LENGTH: 378
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-127-066-42

Query Match Similarity 99.7%; Score 1535; DB 14; Length 378;
 Best Local Similarity 99.6%; Pred. No. 7.8e-120; Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VILSECKTGNGKNGNRGTMKATRQGICWASSSPHRPSPATHPSGLENYCRPDN 60
 Db 6 VVISECKTGNGKNGNRGTMKATRQGICWASSSPHRPSPATHPSGLENYCRPDN 65
 Qy 61 DPOQPWCYTDPERKRYCDILEBECMHCSGENYDKISKTMMSGLBQANDSOPHAH 120
 Db 66 DPOQPWCYTDPERKRYCDILEBECMHCSGENYDKISKTMMSGLBQANDSOPHAH 125
 Qy 121 GYIPSKFPNKLKNYCNPDRLRPWCTTDENKRWLCDIPTCTTPSSGPTYCLK 180
 Db 126 GYIPSKFPNKLKNYCNPDRLRPWCTTDENKRWLCDIPTCTTPSSGPTYCLK 185
 Qy 181 GTGENRYGRGAVAVTWSGHCOHWAQTPHTHERPENFCRNLDENYCRNDSGRAPHCT 240
 Db 186 GTGENRYGRGAVAVTWSGHCOHWAQTPHTHERPENFCRNLDENYCRNDSGRAPHCT 245
 Qy 241 TNSQVRWEVCKLIPSCDSSPV 260
 Db 246 TNSQVRWEVCKLIPSCDSSPV 265

RESULT 15
 US-10-304-287-7

Sequence 7, Application US/10304287
 Publication No. US2003008323A1
 GENERAL INFORMATION:
 APPLICANT: Walsman, David M.
 APPLICANT: Kwon, Mi-jung
 TITLE OF INVENTION: Anti-angiogenesis methods, compositions and uses therefor
 FILE REFERENCE: ME02-001
 CURRENT APPLICATION NUMBER: US/10/304,287
 CURRENT FILING DATE: 2002-11-26
 PRIOR APPLICATION NUMBER: US 60/333,866
 PRIOR FILING DATE: 2001-11-28
 NUMBER OF SEQ ID NOS: 8
 SOFTWARE: Microsoft Word
 SEQ ID NO: 7
 LENGTH: 391
 TYPE: PRT
 ORGANISM: mammalian
 US-10-304-287-7

Query Match Similarity 99.7%; Score 1535; DB 14; Length 391;
 Best Local Similarity 99.6%; Pred. No. 8.1e-120; Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VYLSECKTGNGKNGNRGTMKATRQGICWASSSPHRPSPATHPSGLENYCRPDN 60
 Db 2 VYLSECKTGNGKNGNRGTMKATRQGICWASSSPHRPSPATHPSGLENYCRPDN 61

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OM protein - protein search, using sw model.

Run on: July 27, 2005, 03:24:10 ; Search time 16 Seconds

(without alignments)
1563.522 Million cell updates/sec

Title: US-09-502-176-2

perfect score: 1540

Sequence: 1 VYLSECKTGNGKNYRGTM SK. TNSQVRWEYCKIPSCDSSPV 260

Scoring table: BLOSUM62

Gapop 10.0 , Gapext: 0.5

Searched: 283416 seqs., 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : PIR_79;*

1: pir1;*
2: pir2;*
3: pir3;*
4: pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

1	1535	99.7	810	1	PLHU	plasmin (EC 3.4.21.7) precursor [validated] - human
2	1442	93.5	810	2	B3Q848	plasmin (EC 3.4.21.21)
3	1292	83.9	790	1	PLPG	plasmin (EC 3.4.21.21)
4	1291	83.8	812	1	PLBO	plasmin (EC 3.4.21.21)
5	1274	82.7	812	1	PLMS	plasmin (EC 3.4.21.21)
6	1237	80.3	810	2	I42260	FEBS Lett. 213, 254-260, 1987
7	881	57.2	2869	1	T8518	A;Title: Molecular cloning and characterization of a full-length cDNA clone for human plasminogen, a key proenzyme in the fib.
8	797	51.8	728	1	JH0579	A;Reference number: A35229; MUID:90202879; PMID:2318848
9	782	50.8	728	1	A35644	A;Accession: A35229
10	776.5	50.4	510	1	I42283	A;Molecule type: DNA
11	776	50.4	728	1	A60185	A;Residues: 1-810 <PRT>
12	766.5	49.8	716	1	J5061	A;Cross-references: UNIPROT:P00747; UNIPROT:Q9UBQ9; UNIPROT:Q9UW12; GB:J05286; GB:M34271
13	754.5	49.0	411	2	I41285	A;Status: translated
14	753.5	48.9	716	1	A40332	A;Molecule type: DNA
15	749	48.6	4548	1	S00657	A;Residues: 1-16 <MAIL>
16	739	48.0	711	1	A47136	A;Cross-references: GB:X05199; NID:935530; PID:CAA28831.1; PID:935531
17	739	48.0	1420	2	A2869	A;Experimental source: liver
18	505	32.8	455	2	A61545	R;Malinowski, D.P.; Sadler, J.E.; Davie, E.W.
19	499	32.4	460	2	A61545	Biochemistry, 23, 4243-4250, 1984
20	391.5	25.4	336	2	S33879	A;Title: Characterization of a complementary deoxyribonucleic acid coding for human and
21	372	24.2	625	1	TBBO	A;Cross-references: GB:K02922; MID:9190112; PID:AA60124.1; PID:9387031
22	362.5	23.5	169	2	A60522	A;Accession: 1A5961; MUID:85023311; PMID:6148961
23	357.5	23.2	618	2	A55827	A;Status: translated from GB/EMBL/DBJ
24	351	22.8	622	1	TRU	A;Molecule type: DNA
25	348	22.6	617	2	S10511	A;Residues: 367-419 <MAIL>
26	309.5	20.1	562	1	UKRKT	A;Cross-references: GB:K02921; NID:9190110; PID:AA60123.1; PID:9190111
27	295.5	19.2	559	1	A65029	R;Bruniholz, R.A.; Lierch, P.G.; Schaller, J.; Rickli, B.E.; Lerger, W.; Manneberg, M.
28	281.5	18.3	1	A29941	Bur. J. Biochem. 114, 465-470, 1981	
29	18.1		120	2	B61545	A;Title: Comparison of the primary structure of the N-terminal CNBr fragments of human,

A;Reference number: S03735; MUID:81212097; PMID:7238497
A;Accession: S03735
A;Molecule type: protein
A;Residues: 20-71,'E',73-76

R;Sottrup-Jensen, L.; Petersen, T.B.; Magnusson, S.
Submitted to the ATLAS, July 1977
A;Reference number: A00929
A;Accession: A00929
A;Molecule type: protein
A;Residues: 20-71,'E',73-85,87-105,'D',108-360,'B',362-810 <SOT>
R;Wiman, B.
Bur. J. Biochem. 76, 129-137, 1977
A;Title: Primary structure of the B-chain of human plasmin.
A;Reference number: A04627; MUID:7722545; PMID:142009
A;Molecule type: protein
A;Residues: 581-810 <W1>
R;Wiman, B.; Wallen, P.
Bur. J. Biochem. 50, 489-494, 1975
A;Title: Structural relationship between "glutamic acid" and "lysine" forms of human pla
A;Reference number: A04625; MUID:75093329; PMID:122932
A;Accession: A04625
A;Molecule type: protein
A;Residues: 20-50,'Q',51-71,'E',73-85,87-100 <W12>
R;Wiman, B.; Wallen, P.
Eur. J. Biochem. 58, 539-547, 1975
A;Title: Amino-acid sequence of the cyanogen-bromide fragment from human plasminogen tha
A;Reference number: A04626; MUID:76043692; PMID:126863
A;Accession: A04626
A;Molecule type: protein
A;Residues: 483-507,'B',509-604 <W13>
R;Robins, K.C.; Bernabe, P.; Arzadon, L.; Summaria, L.
J. Biol. Chem. 248, 1631-1633, 1973
A;Title: The primary structure of the active center of human plasmin. II. The histidine loop of human pla
A;Reference number: A92152; MUID:714948; PMID:4694729
A;Contents: annotation; active site
R;Trexler, M.; Vail, Z.; Patti, L.
J. Biol. Chem. 257, 7401-7406, 1982
J. Biol. Chem. 244, 3590-3597, 1969
A;Title: Studies on the active center of human plasmin. Partial amino acid sequence of a
A;Reference number: A92048; MUID:69234739; PMID:424017
A;Contents: annotation; active site
R;Vail, Z.; Patti, L.
J. Biol. Chem. 259, 13630-13694, 1984
A;Title: The fibrin-binding site of human plasminogen. Arginines 32 and 34 are essential
A;Reference number: A92158; MUID:8505494; PMID:609426
A;Contents: annotation; fibrin binding site; omega-aminoacidic acid binding site
R;Cao, Y.; Ji, R.W.; Davidson, D.; Schaller, J.; Marti, D.; Soehnle, S.; McCance, S.G.;
J. Biol. Chem. 271, 2941-2947, 1996
A;Title: Kringle domains of human angiotensin. Characterization of the anti-proliferativ
A;Reference number: A58811; MUID:97067211; PMID:8910613
A;Contents: annotation
R;Lijnen, H.R.; Ugnat, F.; Bini, A.; Collen, D.
Biochemistry 37, 4699-4702, 1998
A;Title: Generation of an angiostatin-like fragment from plasminogen by stromelysin-1 (M
A;Reference number: A58812; MUID:9548733; PMID:9548733
A;Contents: annotation
R;Tulincky, A.; Mulchak, A.M.
submitted to the Brookhaven Protein Data Bank, July 1991
A;Reference number: A51341; PDB:1PK4
A;Contents: annotation; X-ray crystallography, 1.9 angstroms, residues 376-454
R;Tulincky, A.; Wu, T.P.
submitted to the Brookhaven Protein Data Bank, July 1991
A;Reference number: A51488; PDB:2PK4
A;Contents: annotation; X-ray crystallography, 2.25 angstroms, residues 375-454
R;Wu, T.P.; Tulincky, A.
submitted to the Brookhaven Protein Data Bank, August 1993
A;Reference number: A51911; PDB:1PKR
A;Contents: annotation; X-ray crystallography, 2.45 angstroms, residues 102-181
R;Padmanabhan, K.; Tulincky, A.
submitted to the Brookhaven Protein Data Bank, April 1994
A;Reference number: A52408; PDB:1PK
A;Contents: annotation; X-ray crystallography, 2.25 angstroms, residues 377-454
R;Tulincky, A.; Mathews, I.I.
submitted to the Brookhaven Protein Data Bank, December 1995
A;Reference number: A6524; PDB:1CEA
A;Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 102-181
R;Tulincky, A.; Mathews, I.I.
submitted to the Brookhaven Protein Data Bank, December 1995
A;Reference number: A65245; PDB:1CB
A;Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 102-181
R;Mulichak, A.M.; Tulincky, A.; Ravichandran, K.G.
A;Title: Crystal and molecular structure of human plasminogen kringle 4 refined at 1.9
A;Reference number: A58819; MUID:92031502; PMID:1657148
A;Contents: annotation
R;Wu, T.P.; Padmanabhan, K.; Tulincky, A.; Mulichak, A.M.
Biochemistry 30, 10589-10594, 1991
A;Title: The refined structure of the epsilon-aminocaproic acid complex of human plasmi
A;Reference number: A3943; MUID:9118803; PMID:1310033
A;Contents: annotation
R;de Vos, A.M.; Ultsch, R.F.; Padmanabhan, K.; Tulincky, A.; Westbrook, M.
Biochemistry 31, 270-279, 1992
A;Title: Crystal structure of the kringle 2 domain of tissue plasminogen activator at 2
A;Reference number: A58818; MUID:92031503; PMID:1657149
A;Contents: annotation
R;Stec, B.; Reeker, M.M.; Willow, M.; Yamano, A.
submitted to the Brookhaven Protein Data Bank, June 1995
A;Contents: annotation; X-ray crystallography, 2.4 angstroms
R;Rejante, M.; Llinas, M.
submitted to the Brookhaven Protein Data Bank, August 1996
A;Contents: annotation; X-ray crystallography, 1.67 angstroms, residues 376-454
R;Rejante, M.; Llinas, M.
submitted to the Brookhaven Protein Data Bank, August 1996
A;Contents: annotation; conformation by (1)H-NMR, residues 103-181
R;Rejante, M.R.; Llinas, M.
EUR. J. Biochem. 221, 927-937, 1994
A;Title: (1)H-NMR assignments and secondary structure of human plasminogen kringle 1.
A;Reference number: S43645; MUID:9237157; PMID:8181475
A;Contents: annotation; conformation by (1)H-NMR, residues 96-184
R;Rejante, M.R.; Llinas, M.
EUR. J. Biochem. 221, 939-949, 1994
A;Title: Solution structure of the epsilon-aminohexanoic acid complex of human plasmino
A;Reference number: A58817; MUID:9237158; PMID:8181476
A;Contents: annotation; conformation by (1)H-NMR
C;Comment: Plasminogen is synthesized by the kidney and is present in plasma and many o
C;Comment: Plasminogen is converted to plasmin by plasminogen activators (see PIR:UKHU
d PIR:EGHUG)
C;Comment: Plasmin is inactivated by alpha-2-antiplasmin (see PIR:ITHUA2) immediately a
rq-580, resulting in two chains connected by two disulfide bonds. without the inhibitor
C;Comment: Microplasmin is formed by autolytic cleavage of plasmin under artificial con
C;Comment: Stomelysin 1 (see PIR:KCHUS1) acts on plasminogen to produce angiostatin. T
C;Genetic: C
A;Gene: GDB:PLG
A;Cross-references: GDB:119498; OMIM:173350
A;Map position: 6q25-6q27
A;Introns: 17/1; 62/2; 98/1; 136/2; 183/1; 223/2; 263/1; 317/2; 366/1; 419/2; 480/1; 52
C;Function:
A;Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a v
is the walls of the graafian follicle; also activates the urokinase-type plasminogen ac
A;Pathway: fibrinolysis
C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homolog
C;Keywords: angiogenesis inhibitor; blood; duplication; fibrinolysis; glycoprotein; hyd
F1-96-Domain: plasminogen-related protein precursor homology <PUPH>
F1-19-Domain: signal sequence #status predicted <SIG>
F20-810/Product: plasminogen #status experimental <PRO>

F;79-466/Product: angiostatin #status experimental <AST>
 F;97-580, 581-810/Product: plasmin #status experimental <MAT>
 F;03-181/Domain: plasmin chain A #status experimental <CHA>
 F;185-262/Domain: kringle homology <KR1>
 F;377-352/Domain: kringle homology <KR2>
 F;481-550/Domain: kringle homology <KR3>
 F;550-580, 581-810/Product: microplasmin #status experimental <MMT>

Query Match 99.7%; Score 1555; DB 1; Length 810;
 Best Local Similarity 99.6%; Pred. No. 5.6e-104; Indels 1; Gaps 0; Mismatches 239; Conservative 239; Matches 239;

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Qy 1 VYLSECKTGKNGKNGRTGMSKTKGKTCQWSSTSPHRPRFSPATHPSGLEENYCRNPDN 60
Db 98 VYLSECKTGKNGKNGRTGMSKTKGKTCQWSSTSPHRPRFSPATHPSGLEENYCRNPDN 157

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RESULT 2

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Qy 61 DPQGPWCYTDPPEKKYDQDILECBEBCMCGSGENYDGKISKTMGLCQAWDSOPRAH 120
Db 158 DPGCPWCYTDPPEKKYDQDILECBEBCMCGSGENYDGKISKTMGLCQAWDSOPRAH 217

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Qy 121 GYIPSKPKPNKLNKKNYCRNPRLRCPWCTTDPKRWELCDIRCTTPPSSEPTYCLK 180
Db 218 GYIPSKPKPNKLNKKNYCRNPRLRCPWCTTDPKRWELCDIRCTTPPSSEPTYCLK 277

Qy 181 GTGENYRGAVAVTWSGHTQHWSAQTPHTHERPENPCKNLDENYGRAPDGKRPWCHT 240
Db 278 GTGENYRGAVAVTWSGHTQHWSAQTPHTHERPENPCKNLDENYGRAPDGKRPWCHT 337

Qy 241 TNSQVRWEYCKIPSCSSSPV 260
Db 338 TNSQVRWEYCKIPSCSSSPV 357

RESULT 3

```

Qy 241 TNSQVRWEYCKIPSCSSSPV 260
Db 338 TNSQVRWEYCKIPSCSSSPV 357

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Plasmin (EC 3.4.21.7) precursor - pig (fragment)

N/Altenras names: plasminogen

C/Species: miniplasminogen

C/Contains: Sus scrofa domestic pig

C/Date: 07-Sep-1990 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004

C/Accession: S03733; S03737; A25834

R.Brunisholz, R.A.; Schaller, J.; Roosbelet, S.J.; Kaempfer, U.; Rickli, E.E.

Fibrinolysis 1, 91-102, 1987

A/Title: Amino acid sequence of the heavy chain of porcine plasmin. Comparison of the c-terminal fragments of the heavy chain of porcine plasmin and bovine plasmin.

A/Reference number: S03733

A/Accession: S03733

A/Molecule type: protein

A/Residues: 1-360 <SCH>

A/Cross References: UNIPROT:P06867

R.Brunisholz, R.A.; March, P.G.; Schaller, J.; Rickli, E.E.; Lergier, W.; Manneberg, M.

A/Title: Comparison of the primary structure of the N-terminal CNBr fragments of human, bovine and porcine plasmin.

A/Accession: S03737

A/Molecule type: protein

A/Residues: 1-57

R.Marti, T.; Schaller, J.; Rickli, E.E.

Eur. J. Biochem. 149, 279-285, 1985

A/Title: Determination of the complete amino-acid sequence of porcine miniplasminogen.

A/Reference number: A25834; MUID:85203907; PMID:3846533

A/Accession: A25834

A/Molecule type: protein

A/Residues: 450-790 <MAR>

C/Function:

A/Description: dissolves the walls of the graafian follicle; also activates the urokinase-type plasminogen activator pathway.

C/Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology

C/Keywords: fibrinolysis; glycoprotein; hydrolase; kidney; plasma; serine protease

F;1-96/Domain: plasminogen-related protein precursor homology <PLPH>

F;1-9/Domain: signal sequence #status predicted <SIG>

F;10-181/Domain: kringle homology <KR1>

F;185-262/Domain: kringle homology <KR2>

F;275-352/Domain: kringle homology <KR3>

F;377-454/Domain: kringle homology <KR4>

F;481-560/Domain: kringle homology <KR5>

F;581-803/Domain: trypsin homology <TRY>

F;49-53, 61, 103-181, 124-164, 152-176, 188-316, 206-245, 234-257, 275-352, 296-335, 322-622, 665, 780/Active site: His, Asp, Ser #status predicted

Query Match 93.6%; Score 1442; DB 2; Length 810;
 Best Local Similarity 93.1%; Pred. No. 3.1e-97; Indels 0; Gaps 0; Mismatches 242; Conservative 242; Matches 242;

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Qy 1 VYLSECKTGKNGKNGRTGMSKTKGKTCQWSSTSPHRPRFSPATHPSGLEENYCRNPDN 60
Db 98 VYLSECKTGKNGKNGRTGMSKTKGKTCQWSSTSPHRPRFSPATHPSGLEENYCRNPDN 157

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Query Match 83.9%; Score 1292; DB 1; Length 790;
 Best Local Similarity 81.4%; Pred. No. 2.4e-86; Indels 0; Gaps 0; Mismatches 210; Conservative 23; Matches 210;

Qy 61 DPGCPWCYTDPKRWELCDIRCTTPPSSEPTYCLK 277
Db 218 GYIPSKPKPNKLNKKNYCRNPRLRCPWCTTDPKRWELCDIRCTTPPSSEPTYCLK 240

F;561-783/Domain: plasmin chain B #status experimental <BCH>

F;30-54, 34-42, 84-162, 105-145, 133-157, 166-243, 169-297, 187-226, 215-239, 255-333, 277-316, 302-602, 645, 740/Active site: His, Asp, Ser #status predicted

F;602-694, 700-740/Active site: His, Asp, Ser #status predicted

Query Match 83.9%; Score 1292; DB 1; Length 790;
 Best Local Similarity 81.4%; Pred. No. 2.4e-86; Indels 0; Gaps 0; Mismatches 210; Conservative 23; Matches 210;

Qy 1 VYLSECKTGKNGKNGRTGMSKTKGKTCQWSSTSPHRPRFSPATHPSGLEENYCRNPDN 60

RESULT 4

Db 79 IVI~~S~~ECKTGNGNQYRGTSITKSGVICOKWSVSPHPIKSPFKPLAGLENYCRNPDN 138
F;192-269/Domain: kringle homology <KR2>
F;282-359/Domain: kringle homology <KR3>
Oy 61 D~~R~~O~~G~~PW~~C~~T~~D~~P~~K~~R~~V~~YD~~I~~C~~L~~E~~B~~C~~S~~M~~H~~S~~G~~E~~N~~T~~D~~K~~I~~S~~M~~G~~C~~L~~E~~~~Q~~W~~D~~S~~O~~PHAH 120
F;84-461/Domain: kringle homology <KR4>
Db 139 DE~~K~~G~~P~~W~~C~~T~~D~~P~~K~~R~~V~~YD~~I~~C~~L~~E~~B~~C~~S~~M~~H~~S~~G~~E~~N~~T~~D~~K~~I~~S~~M~~G~~C~~L~~E~~~~Q~~W~~D~~S~~O~~PHAH 198
F;84-812/Domain: plamin chain B #status experimental <BCB>
F;56-60-68,110-186,131-171,159-183,192-269,195-323,213-252,241-264,282-359,303-342,3
Oy 121 G~~Y~~I~~P~~S~~K~~F~~P~~N~~K~~N~~K~~KK~~N~~YCR~~N~~P~~D~~R~~L~~R~~P~~C~~F~~T~~D~~P~~K~~W~~E~~L~~C~~I~~P~~R~~C~~T~~P~~P~~S~~G~~P~~T~~Q~~LK 180
F;115/Binding site: carbohydrate (Asn) (covalent) #status experimental
Db 199 G~~Y~~I~~P~~S~~K~~F~~P~~N~~K~~N~~K~~KK~~N~~YCR~~N~~P~~D~~R~~L~~R~~P~~C~~F~~T~~D~~P~~K~~W~~E~~L~~C~~I~~P~~R~~C~~T~~P~~P~~S~~G~~P~~T~~Q~~LK 258
F;65/Binding site: carbohydrate (Ser) (covalent) #status experimental
Oy 181 G~~T~~G~~E~~N~~I~~R~~N~~R~~A~~V~~T~~V~~S~~G~~H~~T~~C~~Q~~H~~N~~S~~A~~Q~~T~~H~~T~~E~~R~~T~~P~~E~~N~~P~~C~~K~~L~~E~~N~~Y~~C~~R~~N~~P~~G~~K~~R~~A~~P~~W~~C~~T~~ 240
A;Description: Cloning and characterization of the bovine plasminogen cDNA.
A;Reference number: S45046
A;Accession: S45046
A;Molecule type: mRNA
A;Residues: 1-812 <BBR>
A;Experimental source: liver
A;Note: it is uncertain whether Met-1 or Met-8 is the initiator
R;Schaller, J.; Moser, P.W.; Damnegger-Muller, G.A.K.; Rosselet, S.J.; Kampfer, U.; Rick
Bur. J. Biochem. 149, 267-278, 1985
A;Title: Complete amino acid sequence of bovine Plasminogen. Comparison with human plasm
A;Accession: A25835
A;Molecule type: protein
A;Residues: 22-334, 'D', 336-515, 'H', 517-554, 'L', 556-812 <SCB>
R;Malinowski, D.P.; Sadier, J.E.; Davie, E.W.
Biochemistry 23, 4243-4250, 1984
A;Title: Characterization of a complementary deoxyribonucleic acid coding for human and
A;Reference number: I45961; MUID:8523311; PMID:148961
A;Accession: I45961
A;Status: translated from GB/EMBL/DDJB
A;Molecule type: mRNA
A;Cross-references: 706-743, 'R', 745-812 <ML>
A;Cross-references: GB;K02935; NID:G163551; PIDN:AAA30714.1; PID:9163552
R;Brunisholz, R.A.; Derci, P.G.; Schaller, J.; Rickli, E.E.; Lergier, W.; Manneberg, M.,
Bur. J. Biochem. 114, 465-470, 1981
A;Title: Comparison of the primary structure of the N-terminal CNBr fragments of human,
A;Reference number: S03735; MUID:81212097; PMID:7238497
A;Accession: S03736
A;Molecule type: protein
A;Residues: 27-83 <BRU>
C;Function:
A;Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a va
ns the wall of the graafian follicle; also activates the urokinase-type plasminogen act
A;Pathway: fibrinolysis
C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
C;Keywords: duplication; fibrinolysis; glycoprotein; hydrolase; kidney; kringle; plasma;
F1-2⁶/Domain: plasminogen-related protein precursor homology <PLPH>
F;8-103/Domain: plasminogen-related protein precursor homology <PLPH>
F;7-812/Product: plasminogen #status experimental <PRO>
F;27-103/Domain: activation peptide #status experimental <APT>
F;04-583; 584-812/Product: plasmin #status experimental <WAT>
F;04-583/Domain: plasmin chain A #status experimental <ACT>
F;10-188/Domain: kringle homology <KR1>
C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homolog

RESULT 5

Db 105 IVI~~S~~ECKTGNGNQYRGTSITKSGVICOKWSVSPHPIKSPFKPLAGLENYCRNPDN 60
F;192-269/Domain: kringle homology <KR2>
F;282-359/Domain: kringle homology <KR3>
Oy 61 D~~R~~O~~G~~PW~~C~~T~~D~~P~~K~~R~~V~~YD~~I~~C~~L~~E~~B~~C~~S~~M~~H~~S~~G~~E~~N~~T~~D~~K~~I~~S~~M~~G~~C~~L~~E~~~~Q~~W~~D~~S~~O~~PHAH 120
F;84-461/Domain: kringle homology <KR4>
Db 165 D~~E~~N~~G~~PW~~C~~T~~D~~P~~K~~R~~V~~YD~~I~~C~~L~~E~~B~~C~~S~~M~~H~~S~~G~~E~~N~~T~~D~~K~~I~~S~~M~~G~~C~~L~~E~~~~Q~~W~~D~~S~~O~~PHAH 224
Oy 121 G~~Y~~I~~P~~S~~K~~F~~P~~N~~K~~N~~K~~KK~~N~~YCR~~N~~P~~D~~R~~L~~R~~P~~C~~F~~T~~D~~P~~K~~W~~E~~L~~C~~I~~P~~R~~C~~T~~P~~P~~S~~G~~P~~T~~Q~~LK 180
F;115/Binding site: carbohydrate (Asn) (covalent) #status experimental
Db 225 G~~Y~~I~~P~~S~~K~~F~~P~~N~~K~~N~~K~~KK~~N~~YCR~~N~~P~~D~~R~~L~~R~~P~~C~~F~~T~~D~~P~~K~~W~~E~~L~~C~~I~~P~~R~~C~~T~~P~~P~~S~~G~~P~~T~~Q~~LK 284
Oy 181 G~~T~~G~~E~~N~~I~~R~~N~~R~~A~~V~~T~~V~~S~~G~~H~~T~~C~~Q~~H~~N~~S~~A~~Q~~T~~H~~T~~E~~R~~T~~P~~E~~N~~P~~C~~K~~L~~E~~N~~Y~~C~~R~~N~~P~~G~~K~~R~~A~~P~~W~~C~~T~~ 240
A;Description: Cloning and characterization of the bovine plasminogen cDNA.
A;Reference number: S45046
A;Accession: S45046
A;Molecule type: mRNA
A;Residues: 1-812 <BBR>
A;Experimental source: liver
A;Note: it is uncertain whether Met-1 or Met-8 is the initiator
R;Schaller, J.; Moser, P.W.; Damnegger-Muller, G.A.K.; Rosselet, S.J.; Kampfer, U.; Rick
Bur. J. Biochem. 149, 267-278, 1985
A;Title: Complete amino acid sequence of bovine Plasminogen. Comparison with human plasm
A;Accession: A25835
A;Molecule type: protein
A;Residues: 22-334, 'D', 336-515, 'H', 517-554, 'L', 556-812 <SCB>
R;Malinowski, D.P.; Sadier, J.E.; Davie, E.W.
Biochemistry 23, 4243-4250, 1984
A;Title: Characterization of a complementary deoxyribonucleic acid coding for human and
A;Reference number: I45961; MUID:8523311; PMID:148961
A;Accession: I45961
A;Status: translated from GB/EMBL/DDJB
A;Molecule type: mRNA
A;Cross-references: 706-743, 'R', 745-812 <ML>
A;Cross-references: GB;K02935; NID:G163551; PIDN:AAA30714.1; PID:9163552
R;Brunisholz, R.A.; Derci, P.G.; Schaller, J.; Rickli, E.E.; Lergier, W.; Manneberg, M.,
Bur. J. Biochem. 114, 465-470, 1981
A;Title: Comparison of the primary structure of the N-terminal CNBr fragments of human,
A;Reference number: S03735; MUID:81212097; PMID:7238497
A;Accession: S03736
A;Molecule type: protein
A;Residues: 27-83 <BRU>
C;Function:
A;Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a va
ns the wall of the graafian follicle; also activates the urokinase-type plasminogen act
A;Pathway: fibrinolysis
C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homolog

RESULT 6

Db 105 IVI~~S~~ECKTGNGNQYRGTSITKSGVICOKWSVSPHPIKSPFKPLAGLENYCRNPDN 60
F;192-269/Domain: kringle homology <KR2>
F;282-359/Domain: kringle homology <KR3>
Oy 61 D~~R~~O~~G~~PW~~C~~T~~D~~P~~K~~R~~V~~YD~~I~~C~~L~~E~~B~~C~~S~~M~~H~~S~~G~~E~~N~~T~~D~~K~~I~~S~~M~~G~~C~~L~~E~~~~Q~~W~~D~~S~~O~~PHAH 120
F;84-461/Domain: kringle homology <KR4>
Db 165 D~~E~~N~~G~~PW~~C~~T~~D~~P~~K~~R~~V~~YD~~I~~C~~L~~E~~B~~C~~S~~M~~H~~S~~G~~E~~N~~T~~D~~K~~I~~S~~M~~G~~C~~L~~E~~~~Q~~W~~D~~S~~O~~PHAH 224
Oy 121 G~~Y~~I~~P~~S~~K~~F~~P~~N~~K~~N~~K~~KK~~N~~YCR~~N~~P~~D~~R~~L~~R~~P~~C~~F~~T~~D~~P~~K~~W~~E~~L~~C~~I~~P~~R~~C~~T~~P~~P~~S~~G~~P~~T~~Q~~LK 180
F;115/Binding site: carbohydrate (Asn) (covalent) #status experimental
Db 225 G~~Y~~I~~P~~S~~K~~F~~P~~N~~K~~N~~K~~KK~~N~~YCR~~N~~P~~D~~R~~L~~R~~P~~C~~F~~T~~D~~P~~K~~W~~E~~L~~C~~I~~P~~R~~C~~T~~P~~P~~S~~G~~P~~T~~Q~~LK 284
Oy 181 G~~T~~G~~E~~N~~I~~R~~N~~R~~A~~V~~T~~V~~S~~G~~H~~T~~C~~Q~~H~~N~~S~~A~~Q~~T~~H~~T~~E~~R~~T~~P~~E~~N~~P~~C~~K~~L~~E~~N~~Y~~C~~R~~N~~P~~G~~K~~R~~A~~P~~W~~C~~T~~ 240
A;Description: Cloning and characterization of the bovine plasminogen cDNA.
A;Reference number: S45046
A;Accession: S45046
A;Molecule type: mRNA
A;Residues: 1-812 <BBR>
A;Experimental source: liver
A;Note: it is uncertain whether Met-1 or Met-8 is the initiator
R;Schaller, J.; Moser, P.W.; Damnegger-Muller, G.A.K.; Rosselet, S.J.; Kampfer, U.; Rick
Bur. J. Biochem. 149, 267-278, 1985
A;Title: Complete amino acid sequence of bovine Plasminogen. Comparison with human plasm
A;Accession: A25835
A;Molecule type: protein
A;Residues: 22-334, 'D', 336-515, 'H', 517-554, 'L', 556-812 <SCB>
R;Malinowski, D.P.; Sadier, J.E.; Davie, E.W.
Biochemistry 23, 4243-4250, 1984
A;Title: Characterization of a complementary deoxyribonucleic acid coding for mouse plasminogen and localization of
A;Reference number: A38514; MUID:9184812; PMID:2081600
A;Accession: A38514
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-812 <BBR>
A;Cross-references: UNIPROT:P20918; GB;J04766; NID:9200402; PIDN:AAA50168.1; PID:920040
R;Liijnen, H.R.; van Heet, B.; Beelen, V.; Collen, D.
Bur. J. Biochem. 224, 861-871, 1994
A;Title: Characterization of the murine plasma fibrinolytic system.
A;Reference number: S48202; MUID:95010076; PMID:7523120
A;Accession: S48202
A;Molecule type: protein
A;Residues: 20-25 <LIU>
A;Accession: S48203
A;Molecule type: protein
A;Residues: 1-812 <BBR>
A;Cross-references: UNIPROT:P20918; GB;J04766; NID:9200402; PIDN:AAA50168.1; PID:920040
R;Liijnen, H.R.; van Heet, B.; Beelen, V.; Collen, D.
Bur. J. Biochem. 224, 861-871, 1994
A;Title: Characterization of the murine plasma fibrinolytic system.
A;Reference number: S48202; MUID:95010076; PMID:7523120
A;Accession: S48202
A;Molecule type: protein
A;Residues: 20-25 <LIU>
A;Accession: S48203
A;Molecule type: protein
A;Residues: 1-812 <BBR>
C;Comment: Plasminogen is synthesized by the kidney and is present in plasma and many o
medically after dissociation from the clot. In the presence of the inhibitor, the activi
e inhibitor, the activation involves also removal of the activation peptide.
C;Comment: Stomelysin 1 (see PRK;KMSS1) acts on plasminogen to produce angiostatin. T
efful in treating solid tumors.
C;Function:
A;Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a v
ns the walls of the graafian follicle; also activates the urokinase-type plasminogen ac
A;Pathway: fibrinolysis
C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homolog

C;Species: Homo sapiens (man)
C;Date: 17-Aug-1992 #text change 17-Aug-1992
C;Accession: JH0579; JU0333; R41140; B36677; A36677; A35512; A19006; PH0114; A37796; S06
R;Seki, T.; Hagiya, M.; Shimomishi, M.; Nakamura, T.; Shimizu, S.
Gene 102, 213-219, 1991
A;Title: Organization of the human hepatocyte growth factor-encoding gene.
A;Reference number: JH0579; MUID:91340155; PMID:1831432
A;Molecule type: DNA
A;Residues: 1-728 <SEK>
A;Cross-references: UNIPROT:P14210; DDBJ:D90318
A;Note: the authors translated the codon GAA for residue 662 as Gly
R;Seki, T.; Hagiya, M.; Shimomishi, M.; Nakamura, T.; Shimizu, S.
submitted to JIPID, March 1991
A;Description: Organization of the human hepatocyte growth factor-encoding gene.
A;Reference number: JU0333
A;Accession: JU0333
A;Molecule type: DNA
A;Residues: 1-481; 'RT' 484-728 <SE2>
R;Weidner, K.M.; Arakaki, N.; Hartmann, G.; Vandekerckhove, J.; Weingart, S.; Rieder, H.
Proc. Natl. Acad. Sci. U.S.A. 88, 7001-7005, 1991.
A;Title: Evidence for the identity of human scatter factor and human hepatocyte growth factor
A;Reference number: A41140; MUID:9134393; PMID:1831266
A;Accession: A41140
A;Molecule type: mRNA
A;Residues: 1-728 <WEI>
A;Cross-references: GB:M73239; NID:9337935; PIDN:AAA64239.1; PID:9337935
R;Seki, T.; Ihara, I.; Sugimura, A.; Shimomishi, M.; Nishizawa, T.; Asami, O.; Hagiya, M.
Biochem. Biophys. Res. Commun. 172, 321-327, 1990
A;Title: Isolation and expression of cDNA for different forms of hepatocyte growth factor
A;Reference number: A36677; MUID:91025062; PMID:2145536
A;Accession: B36677
A;Residues: 1-728 <SE3>
A;Cross-references: GB:M67018; NID:9184031; PIDN:AA52648.1; PID:9184032
A;Accession: A36677
A;Molecule type: mRNA
A;Residues: 1-161; 167-728 <SE4>
A;Cross-references: EMBL:X16323
A;Experimental source: leukocyte
R;Miyazawa, K.; Tsubouchi, H.; Naka, D.; Takahashi, K.; Okigaki, M.; Arakaki, N.; Nakaya
Biochem. Biophys. Res. Commun. 163, 967-973, 1989
A;Title: Molecular cloning and sequence analysis of cDNA for human hepatocyte growth factor
A;Reference number: AJ3512; MUID:89392017; PMID:2528952
A;Accession: AJ3512
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-728 <MTY>
A;Cross-references: GB:M29145; NID:9184041; PIDN:AA52650.1; PID:9306846
R;Rubin, J.S.; Chan, A.M.L.; Bottaro, D.P.; Burgess, W.H.; Taylor, W.G.; Cech, A.C.; Hir
Proc. Natl. Acad. Sci. U.S.A. 88, 415-419, 1991
A;Title: A broad-spectrum human lung fibroblast-derived mitogen is a variant of hepatocyte
A;Accession: AJ39006; MUID:9110540; PMID:1824873
A;Accession: AJ39006
A;Molecule type: mRNA
A;Residues: 1-161; 167-728 <RUB>
A;Cross-references: GB:MS5379
A;Experimental source: embryonic lung
R;Yoshimaya, Y.; Arakaki, N.; Naka, D.; Takahashi, K.; Hiroto, J.; Nakayama,
Biochem. Biophys. Res. Commun. 175, 660-667, 1991
A;Title: Identification of the N-terminal residue of the heavy chain of both native and
A;Reference number: PH0114; MUID:91207365; PMID:1826837
A;Accession: PH0114
A;Molecule type: protein
A;Residues: 32-43; 53-58 <YOS>
A;Experimental source: plasma
R;Weidner, K.M.; Behrens, J.; Vandekerckhove, J.; Birchmeier, W.
J. Cell Biol. 111, 2057-2108, 1990
A;Title: Scatter factor: molecular characteristics and effect on the invasiveness of epi
A;Reference number: A37796; MUID:91035621; PMID:2146276
A;Accession: A37796
A;Molecule type: protein
A;Residues: 86-91; 329-344; 356-363; 'XX' 366-370; 425-434; 442-447; 'X' 449-450; 543-546; 'X', 5

R; Nakamura, T.; Nishizawa, T.; Hagiya, M.; Seki, T.; Shimoniishi, M.; Sugimura, A.; Tashiro, K.; Nature 342, 440-443, 1989
A; Title: Molecular cloning and expression of human hepatocyte growth factor.
A; Reference number: S06794; MUID:9066676; PMID:2531289
A; Accession: S06794
A; Molecule type: mRNA
A; Residues: 1-31, 'H³', 34-77, 'N', 79-292, 'V', 294-299, 'W', 301-316, 'A', 318-335, 'K', 337-386,
A; Cross-references: EMBL:X16233; NID:932081; PIDN:CAA34387_1; PID:932082
A; Experimental source: liver
A; Note: the authors translated the codon CAG for residue 727 as Glu
A; Note: part of this sequence, including the amino end of both the alpha and beta chains
R; Harrmann, G.; Nardini, L.; Weider, K.M.; Sachs, M.; Vigna, E.; Comoglio, P.M.; Birch, J.; Proc. Natl. Acad. Sci. U.S.A. 89, 11574-11578, 1992
A; Title: A functional domain in the heavy chain of scatter factor/hepatocyte growth factor
A; Reference number: I59214; MUID:9308751; PMID:1208030
A; Accession: I59214
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-288, 'ET', <HAR>
A; Cross-references: GB:I02931; NID:918033; PIDN:AAA2649_1; PID:918034
R; Miyazawa, K.; Kitamura, A.; Naka, D.; Kitamura, N.
Eur. J. Biochem. 197, 15-22, 1991
A; Title: An alternatively processed mRNA generated from human hepatocyte growth factor
A; Reference number: S15443; MUID:9120041; PMID:1826653
A; Accession: S15443
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-288, 'ET', <MIY2>
A; Cross-references: EMBL:X57574; NID:932083; PIDN:CAA40802_1; PID:932084
R; Shima, N.; Nagao, M.; Ogaki, F.; Tsuda, E.; Mirakami, A.; Higashio, K.
Biochem. Biophys. Res. Commun. 180, 1151-1158, 1991
A; Title: Tumor cytotoxic factor/hepatocyte growth factor from human fibroblasts: cloning
A; Reference number: I52253; MUID:92062055; PMID:1835383
A; Accession: I52253
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 161-166 <SHI>
A; Cross-references: GB:S62561; NID:9237996; PIDN:AAB20169_1; PID:9237997
A; Geno: GB:HGF
C; Genetics:
A; Map position: 7q21.1-'q21.1
A; Introns: 30/1; 85/2; 123/1; 161/2; 209/1; 249/2; 289/1; 347/2; 390/1; 424/2; 469/1; 4
C; Function: disulfide-bonded heterodimer of chains derived from the same precursor
C; Description: stimulates mitosis of hepatocytes and other cells
A; Note: does not have protease activity
C; Superfamily: hepatocyte growth factor/macrophage stimulating protein 1; kringle homolog
C; Keywords: alternative splicing; glycoprotein; growth factor; heterodimer; kringle; pyruvate
F; 1-31/*Domain: signal sequence #status predicted <SIG>
F; 32-49/*Domain: hepatocyte growth factor #status experimental <MAT>
F; 32-49/*Domain: alpha chain #status experimental <ACH>
F; 128-206/*Domain: kringle homology <KR1>
F; 211-286/*Domain: kringle homology <KR2>
F; 303-383/*Domain: kringle homology <KR3>
F; 391-469/*Domain: kringle homology <KR4>
F; 455-726/*Domain: beta chain #status experimental <BCB>
F; 495-726/*Domain: beta chain #status experimental <TRX>
F; 32/*Modified site: pyrrolidine carboxylic acid (Gln) (in mature form) #status experimental
F; 234, 402, 665, 653/*Binding site: carbohydrate (Asn) (covalent) #status predicted
F; 487-604/*Disulfide bonds: Hettatus predicted

Query Match 51.8%; Score 797; DB 1; Length 728;
Best Local Similarity 51.0%; Pred. No. 1.8e-50; Matches 134; Conservative 42; Mismatches 81; Indels 6; Gaps 4;

Qy	2	VLSCECTGNGKNGYRGTMKSITKGKQPSMSPHESFLPSSVRGGDQENYCRNPND
Db	124	YIRNCIGKGSYKCYTISITKGKQPSMSPHESFLPSSVRGGDQENYCRNPND
	:	: : : : : : : : : :
	62	POGPWYTTPEKRYTDICLREC-BECMCSGENYDGKISKMSGLECAWDSSOPHAN
Oy	184	EGGPWPFISHTSPEVRLTCVCDIPQCSVECHTCNGSYRGMDHTESGKICORWDQIPHRH

183
120
243

QY	121 GYIISKFPNKLKQYCRNPDRRLRPWCTTDPNKRWECLIDPRT-----TPPPSGP 176	Db	245 KFLPERYPDQFDNDTCRNPDGKPRPWCYLDPDTPWYCAIKCNAISAVNETDVPE-- 302
QY	244 KFLPERYPDQFDNDTCRNPDGKPRPWCYLDPDTPWYCAIKTCADNTKNDTDPLETT 303	Db	245 KFLPERYPDQFDNDTCRNPDGKPRPWCYLDPDTPWYCAIKCNAISAVNETDVPE-- 302
QY	177 QCKIKGTYGNGVAVTWSGHTCQHWAQTPHTHERTPENFPCNLDENYCRNPDKGR 236	Db	303 TIECIKGQGEGYRGTTINTWIGIPCRWDQSPHKAIDTPENFKCOLRENTCRNPDPGAE 362
QY	304 ECTQGSGYRGTTINTWIGIPCRWDQSPHKAIDTPENFKCOLRENTCRNPDPGESP 363	Db	303 TIECIKGQGEGYRGTTINTWIGIPCRWDQSPHKAIDTPENFKCOLRENTCRNPDPGAE 362
QY	237 WCHTNTNSQVRWEYC-KIPSCDSS 258	Db	335 APWCHTNTNSQVRWEYC-KIPSCDSS 258
QY	364 WCTTDPKIRVGKCSQIPNCDMS 386	Db	363 SPWCFTDPNIRVGKCSQIPKCDVS 387
RESULT 9			
A35644	hepatocyte growth factor precursor - rat	N;Alternate names:	hepapoietin A; scatter factor
C;Species:	Rattus norvegicus (Norway rat)	C;Accession:	A35644; S1321
C;Date:	28-Sep-1990 #sequence_revision 18-Nov-1992 #text_change 09-Jul-2004	C;Date:	13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-May-2004
C;Accession:	A35644; S1321	R;Nakamura, H.; Tashiro, K.; Nakamura, T.; Shiokawa, K.	Mech. Dev. 49, 123-131, 1995.
R;Okajima, A.; Miyazawa, K.; Kitamura, N.	Bur. J. Biochem. 139, 375-381, 1990	A;Title:	Molecular cloning of Xenopus HGF cDNA and its expression studies in Xenopus eggs.
A;Reference number:	Proc. Natl. Acad. Sci. U.S.A. 87, 3200-3204, 1990	A;Accession number:	I51283; MUID:95267650; PMID:7748783
A;Title:	Deduced primary structure of rat hepatocyte growth factor and expression of the gene	A;Status:	preliminary;
A;Reference number:	A35644; MUID:90222197; PMID:2139229	A;Accession:	A35644
A;Status:	preliminary	A;Molecule type:	mRNA
A;Molecule type:	mRNA	A;Residues:	1-728 <OKA>
A;Residues:	1-728 <OKA>	A;Cross-references:	EMBL:X54400; NID:956353; PIDN:CAA382661; PID:94539554
A;Cross-references:	UNIPROT:P17945; GB:D90102; GB:M32987; NID:9220766; PIDN:BA141331; PIDN:BA141331.1; PIDN:BA141331.2	A;Note:	the authors translated the codon GAG for residue 70 as Gln, GAC for residue 417
A;Cross-references:	UNIPROT:P17945; GB:D90102; GB:M32987; NID:9220766; PIDN:BA141331; PIDN:BA141331.1; PIDN:BA141331.2	C;Complex:	disulfide-bonded heterodimer of chains derived from the same precursor
A;Cross-references:	UNIPROT:P17945; GB:D90102; GB:M32987; NID:9220766; PIDN:BA141331; PIDN:BA141331.1; PIDN:BA141331.2	C;Function:	
A;Cross-references:	UNIPROT:P17945; GB:D90102; GB:M32987; NID:9220766; PIDN:BA141331; PIDN:BA141331.1; PIDN:BA141331.2	A;Description:	stimulates mitosis of hepatocytes and other cells
A;Cross-references:	UNIPROT:P17945; GB:D90102; GB:M32987; NID:9220766; PIDN:BA141331; PIDN:BA141331.1; PIDN:BA141331.2	A;Note:	does not have protease activity
A;Cross-references:	UNIPROT:P17945; GB:D90102; GB:M32987; NID:9220766; PIDN:BA141331; PIDN:BA141331.1; PIDN:BA141331.2	C;Superfamily:	hepatocyte growth factor/macrophage stimulating protein 1; kringle homology
A;Cross-references:	UNIPROT:P17945; GB:D90102; GB:M32987; NID:9220766; PIDN:BA141331; PIDN:BA141331.1; PIDN:BA141331.2	C;Keywords:	duplication; glycoprotein; growth factor; heterodimer; kringle homology
A;Cross-references:	UNIPROT:P17945; GB:D90102; GB:M32987; NID:9220766; PIDN:BA141331; PIDN:BA141331.1; PIDN:BA141331.2	F;42-477, 478-709/Product:	hepatocyte growth factor #status predicted <NAT>
A;Cross-references:	UNIPROT:P17945; GB:D90102; GB:M32987; NID:9220766; PIDN:BA141331; PIDN:BA141331.1; PIDN:BA141331.2	F;42-477/Domain:	hepatocyte growth factor alpha chain #status predicted <ACH>
A;Cross-references:	UNIPROT:P17945; GB:D90102; GB:M32987; NID:9220766; PIDN:BA141331; PIDN:BA141331.1; PIDN:BA141331.2	F;115-193/Domain:	kringle homology <KR1>
A;Cross-references:	UNIPROT:P17945; GB:D90102; GB:M32987; NID:9220766; PIDN:BA141331; PIDN:BA141331.1; PIDN:BA141331.2	F;198-275/Domain:	kringle homology <KR2>
A;Cross-references:	UNIPROT:P17945; GB:D90102; GB:M32987; NID:9220766; PIDN:BA141331; PIDN:BA141331.1; PIDN:BA141331.2	F;219-367/Domain:	kringle homology <KR3>
A;Cross-references:	UNIPROT:P17945; GB:D90102; GB:M32987; NID:9220766; PIDN:BA141331; PIDN:BA141331.1; PIDN:BA141331.2	F;478-709/Domain:	hepatocyte growth factor beta chain #status predicted <TRY>
A;Cross-references:	UNIPROT:P17945; GB:D90102; GB:M32987; NID:9220766; PIDN:BA141331; PIDN:BA141331.1; PIDN:BA141331.2	F;478-709/Domain:	trypsin homology <TRY>
A;Cross-references:	UNIPROT:P17945; GB:D90102; GB:M32987; NID:9220766; PIDN:BA141331; PIDN:BA141331.1; PIDN:BA141331.2	F;470-589/Disulfide bonds:	#status predicted
RESULT 10			
151283	hepatocyte growth factor precursor - clawed frog	N;Alternate names:	hepapoietin A; scatter factor
R;Nakamura, H.; Tashiro, K.; Nakamura, T.; Shiokawa, K.	Mech. Dev. 49, 123-131, 1995.	C;Species:	Xenopus sp. (clawed frog)
R;Nakamura, H.; Tashiro, K.; Nakamura, T.; Shiokawa, K.	A;Title:	Molecular cloning of Xenopus HGF cDNA and its expression studies in Xenopus eggs.	
R;Nakamura, H.; Tashiro, K.; Nakamura, T.; Shiokawa, K.	A;Accession number:	I51283; MUID:95267650; PMID:7748783	
R;Nakamura, H.; Tashiro, K.; Nakamura, T.; Shiokawa, K.	A;Status:	preliminary; translated from GB/EMBL/DDJ	
R;Nakamura, H.; Tashiro, K.; Nakamura, T.; Shiokawa, K.	A;Molecule type:	mRNA	
R;Nakamura, H.; Tashiro, K.; Nakamura, T.; Shiokawa, K.	A;Residues:	1-710 <NAK>	
R;Nakamura, H.; Tashiro, K.; Nakamura, T.; Shiokawa, K.	A;Cross-references:	GB:S77422; NID:9998932; PIDN:ABA34354.1; PID:9998933	
R;Nakamura, H.; Tashiro, K.; Nakamura, T.; Shiokawa, K.	A;Note:	the authors' translation for residue 458 (Thr) is inconsistent with the nucleic acid sequence	
R;Nakamura, H.; Tashiro, K.; Nakamura, T.; Shiokawa, K.	C;Complex:	disulfide-bonded heterodimer of chains derived from the same precursor	
R;Nakamura, H.; Tashiro, K.; Nakamura, T.; Shiokawa, K.	C;Function:		
R;Nakamura, H.; Tashiro, K.; Nakamura, T.; Shiokawa, K.	A;Description:	stimulates mitosis of hepatocytes and other cells	
R;Nakamura, H.; Tashiro, K.; Nakamura, T.; Shiokawa, K.	A;Note:	does not have protease activity	
R;Nakamura, H.; Tashiro, K.; Nakamura, T.; Shiokawa, K.	C;Superfamily:	hepatocyte growth factor/macrophage stimulating protein 1; kringle homology	
R;Nakamura, H.; Tashiro, K.; Nakamura, T.; Shiokawa, K.	C;Keywords:	duplication; glycoprotein; growth factor; heterodimer; kringle homology	
R;Nakamura, H.; Tashiro, K.; Nakamura, T.; Shiokawa, K.	F;42-477, 478-709/Product:	hepatocyte growth factor #status predicted <NAT>	
R;Nakamura, H.; Tashiro, K.; Nakamura, T.; Shiokawa, K.	F;42-477/Domain:	hepatocyte growth factor alpha chain #status predicted <ACH>	
R;Nakamura, H.; Tashiro, K.; Nakamura, T.; Shiokawa, K.	F;115-193/Domain:	kringle homology <KR1>	
R;Nakamura, H.; Tashiro, K.; Nakamura, T.; Shiokawa, K.	F;198-275/Domain:	kringle homology <KR2>	
R;Nakamura, H.; Tashiro, K.; Nakamura, T.; Shiokawa, K.	F;219-367/Domain:	kringle homology <KR3>	
R;Nakamura, H.; Tashiro, K.; Nakamura, T.; Shiokawa, K.	F;478-709/Domain:	hepatocyte growth factor beta chain #status predicted <TRY>	
R;Nakamura, H.; Tashiro, K.; Nakamura, T.; Shiokawa, K.	F;52-128, 281-322, 379, 556, 637, 666/Binding site:	carbohydrate (Asn) (covalent) #status predicted <BCN>	
R;Nakamura, H.; Tashiro, K.; Nakamura, T.; Shiokawa, K.	F;470-589/Disulfide bonds:	#status predicted	
RESULT 11			
QY	Query Match 50.4%; Score 765; DB 1; Length 710; Best Local Similarity 50.0%; Freq. No. 5.4e-49; Matches 132; Conservative 39; Mismatches 84; Indels 10; Gaps 4;	Db	245 KFLPERYPDQFDNDTCRNPDGKPRPWCYLDPDTPWYCAIKCNAISAVNETDVPE-- 302
QY	2 YLSECKTGNGKNGYRGTMKNGTICQKNSSTSPPHRPRSPATHPSEGLEYCNPND 61	Db	244 KFLPERYPDQFDNDTCRNPDGKPRPWCYLDPDTPWYCAIKTCADNTKNDTDPLETT 303
QY	111 YIRDQTHGKNSNGYRGTRNTRVKGLAGQPNMSMIPIHESELSTYRKDQKLNENCPKG 170	Db	171 BGGPWCYTDPBKRYDCILEEC-BEHCISGENGDGKISKIMSGLEQAWMSQSPAH 120
QY	62 FOGPWCYTDPBKRYDCILEEC-BEHCISGENGDGKISKIMSGLEQAWMSQSPAH 120	Db	121 GYIISKFPNKLKQYCRNPDRRLRPWCTTDPNKRWECLIDPRT-----TPPPSGP 179
QY	171 YRNCNIGKGSYKTKGVTSKRGKCKQPNMSMIPHEHLPSLSSRKGKQDQENYCRNPGE 184	Db	231 KGYIISKFPNKLKQYCRNPDRRLRPWCTTDPNKRWECLIDPRT-----TPPPSGP 179
QY	184 EGCPWCFTSNEPVYEVCDIPOCSVECMTCNGSYRGPMHDTEGKTCRQWDQPTPHK 244	Db	231 KGYIISKFPNKLKQYCRNPDRRLRPWCTTDPNKRWECLIDPRT-----TPPPSGP 179
QY	185 EGCPWCFTSNEPVYEVCDIPOCSVECMTCNGSYRGPMHDTEGKTCRQWDQPTPHK 244	Db	351 TTDPNIRGHQSOIKKCOAS 370
QY	121 GYIISKFPNKLKQYCRNPDRRLRPWCTTDPNKRWECLIDPRT-----TPPPSGP 174	Db	351 TTDPNIRGHQSOIKKCOAS 370
QY	60185 RESULT 11	Db	351 TTDPNIRGHQSOIKKCOAS 370

N;Alternate name: hepatoprotein A; scatter factor
 C;Species: Mus musculus (house mouse)
 C;Date: 03-Mar-1993 #sequence_revision 26-May-1994 #text_change 09-Jul-2004
 C;Accession: JCC117; P2064; A60185; S45416; S17173; S10966; I48758; JU0231
 R;Sasaki, M.; Nishio, M.; Sasaki, T.; Enami, J.
 Biochem. Biophys. Res. Commun. 199, 772-779, 1994
 A;Title: Identification of mouse mammary fibroblast-derived mammary growth factor as heparin homology protein
 A;Reference number: JCC117; MUID:94183257; PMID:8135822
 A;Molecule type: mRNA
 A;Residues: 1-228 <SAS>
 A;Cross-references: UNIPROT:Q08048; GB:D10212; NID:9220435; PIDN:BA01064.1; PID:9220436
 A;Experimental source: fibroblast, COS-1 cell
 A;Note: submitted to JIPID, May 1993
 A;Accession: P22064
 A;Molecule type: protein
 A;Residues: 495-504 <SA2>
 R;Rosen, E.M.; Melonsky, L.; Setter, B.; Vinter, D.W.; Goldberg, I.D.
 Proc. Soc. Exp. Biol. Med. 195, 3443, 1990
 A;Title: Purified scatter factor simulates epithelial and vascular endothelial cell migration
 A;Reference number: A60185; MUID:90377927; PMID:2144630
 A;Accession: A60185
 A;Molecule type: protein
 A;Residues: 'X', 184-188, 'KX', 191-192, 'X', 194-'XX', 197-357-364, 'XX', 367-375-377, 'E', 379-'
 R;Liu, Y.; Michalopoulos, G.K.; Zarnegar, R.
 Biochim. Biophys. Acta 1216, 299-319, 1993
 A;Title: Molecular cloning and characterization of cDNA encoding mouse hepatocyte growth factor
 A;Reference number: S43416; MUID:94060105; PMID:8241272
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Cross-references: EMBL:X72307
 R;Liu, Y.
 submitted to the EMBL Data Library, May 1993
 A;Reference number: S45521
 A;Accession: S45521
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-563, 'H', 565-728 <LIU>
 A;Cross-references: EMBL:X72207
 R;Coffer, A.; Fellows, J.; Young, S.; Pappin, D.; Rahman, D.
 Biochem. J. 278, 35-41, 1991
 A;Title: Purification and characterization of biologically active scatter factor from rat liver
 A;Reference number: S17173; MUID:91354223; PMID:1831975
 A;Accession: S17173
 A;Molecule type: protein
 A;Residues: 495-517, 'T', 519 <COF>
 Nature 346, 228, 1990
 A;Title: Hepatocytes and scatter factor
 A;Reference number: S10966; MUID:90326152; PMID:2142751
 A;Accession: S10966
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 496-507, 'X', 509-512, 'L', 514-516, 'X', 518-519 <NAT>
 R;Plaschke-Schlutter, A.; Behrens, J.; Gherardi, E.; Bircheimer, W.
 J. Biol. Chem. 270, 830-836, 1995
 A;Title: Characterization of the scatter factor/hepatocyte growth factor gene promoter.
 A;Reference number: I48758; MUID:9512532; PMID:7822218
 A;Accession: I48758
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-30 <RES>
 A;Cross-references: EMBL:X81630; NID:9673451; PIDN:CA57286.1; PID:9673452
 C;Complex: disulfide-bonded heterodimer of chains derived from the same precursor
 C;Description: stimulates mitosis of hepatocytes and other cells
 A;Note: does not have protease activity
 C;Superfamily: hepatocyte growth factor/macrophage stimulating protein 1; kringle homologous domain
 C;Keywords: alternative splicing; glycoprotein; growth factor; heterodimer; kringle; pyrantel F1-32; domain; signal sequence #status predicted <SIG>
 F1-32-488-489-716/Domain: macrophage-stimulating protein 1 alpha chain #status predicted <MMT>
 F1-32-488/Domain: macrophage-stimulating protein 1 alpha chain #status predicted <ACH>
 F1-110-186/Domain: kringle homology <KR1>
 F1-191-268/Domain: kringle homology <KR2>
 F1-292-370/Domain: kringle homology <KR3>
 F1-379-457/Domain: kringle homology <KR4>
 F1-489-716/Domain: macrophage-stimulating protein 1 beta chain #status predicted <BCH>
 F1-489-709/Domain: trypsin homology <TRY>
 F1-72, 305, 620/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 50.4%; Score 776; DB 1; Length 728;
 Best Local Similarity 49.4%; Pred. No. 6e-49; Mismatches 84; Indels 10; Gaps 4;
 Matches 132; Conservative 35; MisMatches 89; Indels 15; Gap 5;
 Qy 2 YLSECKTGNGKNGYRGMSKTGNGTCOKNSSTSPPHRPRSPATHSEGILEENYCRNPND 61
 Db 106 VVTCIMDNGASYRGVARTADGLPCQAMSRRFPNDHKIPT-PKNGQBNFCRNPDGD 163
 Fv 488-607/Disulfide bonds: #status predicted

Query Match RESULT 12
 Best Local Similarity 49.4%; Pred. No. 6e-49; Mismatches 84; Indels 10; Gaps 4;
 Matches 132; Conservative 35; MisMatches 89; Indels 15; Gap 5;
 Qy 2 YLSECKTGNGKNGYRGMSKTGNGTCOKNSSTSPPHRPRSPATHSEGILEENYCRNPND 61
 Db 125 YLSECKTGNGKNGYRGMSKTGNGTCOKNSSTSPPHRPRSPATHSEGILEENYCRNPND 61
 Fv 62 POGPWCYTDPKRYDVGDLCEEC-BCHMCGSGENTYDGKISKTMGSLCQAWDSQSPAH 120
 Db 185 EGPPWCFTFSNPVEYEVCDIPOCSEVECWTGNGESTFRGPMDHTESGKTCORWDQQPHR 244
 Qy 121 GYPSKFKENPKLNKKNYCRNPDELRPWCFTDPKNGKELCDPCT----TPPSSGP 174
 Db 245 KFLPERVPDKGFDDNYCHNPDKGPCKPRPWYTYLDPDTPEWYCAIKTCAHSAVNETDVME-- 302
 Qy 175 TYQCLKGSGENTYGRNVAWVNSGHTCWAHSQTPHTHERTPENPCKNLDENYCRNDGKR 234
 Db 303 TWCIOQSGEGGRGTSITWICPQRCWDSQYPHKNDITPENFKCDLRENYCRNDGAE 362
 Qy 235 APNCHTNNSQVWEMYC-KIPSQDS 258
 Db 363 SPACFTDPNIRVGYCSQIPKCDVS 387

Query Match RESULT 13
 Best Local Similarity 49.4%; Pred. No. 6e-49; Mismatches 84; Indels 10; Gaps 4;
 Matches 132; Conservative 35; MisMatches 89; Indels 15; Gap 5;
 Qy 2 YLSECKTGNGKNGYRGMSKTGNGTCOKNSSTSPPHRPRSPATHSEGILEENYCRNPND 61
 Db 125 YLSECKTGNGKNGYRGMSKTGNGTCOKNSSTSPPHRPRSPATHSEGILEENYCRNPND 61
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 09-Jul-2004
 C;Accession: JCC061
 R;Ohshiro, K.; Iwama, A.; Matsuno, K.; Ezaki, T.; Sakamoto, O.; Hamaguchi, I.; Takasu, A.;Biochem. Biophys. Res. Commun. 227, 273-280, 1996
 A;Title: Molecular cloning of rat macrophage-stimulating protein and its involvement in A;Reference number: JCC061; MUID:9701126; PMID:8858156
 A;Accession: JCC061
 A;Molecule type: mRNA
 A;Residues: 1-716 <OHS>
 A;Cross-references: UNIPROT:P0521; EMBL:X95096; NID:91669718; PIDN:CAA64473.1; PID:916 C;Complex: disulfide-bonded heterodimer of chains derived from the same precursor
 C;Superfamily: hepatocyte growth factor/macrophage stimulating protein 1; kringle homologous domain
 C;Keywords: duplication; glycoprotein; growth factor; kringle homologous domain
 F1-1-31/Domain: signal sequence #status predicted <SIG>
 F1-32-488-489-716/Domain: macrophage-stimulating protein 1 alpha chain #status predicted <MMT>
 F1-32-488/Domain: macrophage-stimulating protein 1 alpha chain #status predicted <ACH>
 F1-110-186/Domain: kringle homology <KR1>
 F1-191-268/Domain: kringle homology <KR2>
 F1-292-370/Domain: kringle homology <KR3>
 F1-379-457/Domain: kringle homology <KR4>
 F1-489-716/Domain: macrophage-stimulating protein 1 beta chain #status predicted <BCH>
 F1-489-709/Domain: trypsin homology <TRY>
 F1-72, 305, 620/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match RESULT 14
 Best Local Similarity 49.4%; Pred. No. 2.9e-48; Mismatches 89; Indels 15; Gap 5;
 Matches 132; Conservative 35; MisMatches 89; Indels 15; Gap 5;

RESULT 13

151285 -hepatocyte growth factor/scatter factor - chicken (fragment)
 C;Species: Gallus gallus (chicken)
 C;Date: 11-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
 C;Accession: I51285
 R;Strcrit: A.; Stern, C.D.; Thery, C.; Ireland, G.W.; Aparicio, S.; Sharpe, M.J.; Gherard Development 121, 811-824, 1995
 A;Title: A role for HGF/SF in neural induction and its expression in Hensen's node durin
 A;Reference number: 151285; MUID:95237013; PMID:7720585
 A;Status: Preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-411 <SR>
 A;Cross-references: UniProt:Q90978; GB:S77480; NID:998675; PID:998676
 C;Supporting family: hepatocyte growth factor/macrophage stimulating protein 1; kringle homolog
 F;124-197/Domain: kringle homology <KRG>
 F;202-279/Domain: kringle homology <KR2>
 F;295-374/Domain: kringle homology <KR3>

Query Match 49.0%; Score 754.5; DB 2; Length 411;
 Best Local Similarity 50.2%; Pred. No. 1.2e-47;
 Matches 132; Conservative 31; Mismatches 89; Indels 11; Gaps 4;

Qy 2 XISECKTGNGKNGYRGTMSKTKITCOKWSNSPHPRFSPATHPSEGLEYCRNPND 61
 Db 120 YRNCLIGKGAKYKGITSITSGIQCWNNSPIHE---HSYRGKDLRENNYCRNPRGE 174

Qy 62 PGGPWCVTTPDKRYDPCILECEB-ECMHESGENGDGKISKITMSLGEQAWDSOPHAH 120
 Db 175 EGGPWCFPTSTPSMRHEVCDIPLCSEVECMTCNGESTRGPMHTEGSKECQWDLGRPKH 234

Qy 121 GYPSKEPNKQKKNQCNPDRBLRWCFTDPNKRCWELCDIPRCITPPSS---GPTY 176
 Db 235 KFRPERYPDKEFDNYCRNPKURPFCITDPNTFWEFCIKTCVGILNSTEAATT 294

Qy 177 QCLKGKGTGNGYRGNVAVTWSGICQHNSAQTHTHTBETPENPKQNDENYCRNPQKRAP 236
 Db 295 TCIQGEGEGYRVTNTIWSGICQQRNDSQFPHONHTPENFKCOLRENYCRNPQSESP 354

Qy 237 WCHTTNSQVRMYC-KIPSCSS 258
 Db 355 WCFPTDPNIRIGYCSQPKCBVS 377

RESULT 14

A40332 macrophage-stimulating protein 1 precursor - mouse
 N;Alternate names: hepatocyte growth factor-like protein
 C;Species: Mus musculus (house mouse)
 C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
 C;Accession: A40332; B40332
 R;Degen, S.J. F.; Stuart, L.A.; Han, S.; Jamison, C.S.
 Biochemistry 30, 9781-9791, 1991
 A;Title: Characterization of the mouse cDNA and gene coding for a hepatocyte growth fact
 A;Reference number: A40332; MUID:92002017; PMID:1832957
 A;Accession: A40332

Query Match 48.9%; Score 753.5; DB 1; Length 716;
 Best Local Similarity 48.3%; Pred. No. 2.5e-47;
 Matches 129; Conservative 37; Mismatches 86; Indels 15; Gaps 5;

Qy 2 YLSBCKTGNGKNGYRGTMSKTKITCOKWSNSPHPRFSPATHPSEGLEYCRNPND 61
 Db 106 YVRLCKTGNGKNGYRGTMSKTKITCOKWSNSPHPRFSPATHPSEGLEYCRNPND 61
 Qy 62 PGGWCYTTPDKRYDPCILECEB-ECHGSGENYDGKISKITMSLGEQAWDSOPHAH 120
 Db 164 PRGPWCYTTSNSVRSFVOSCGKIKTREREAVCWLNGEDYRVDVTESGRCQRMQLQHPISH 223

Qy 121 GYPSKEPNKQKKNQCNPDRBLRWCFTDPNKRCWELCDIPRCITPPSS---GPTY 176
 Db 224 PFQBFKFLDKDKYDNQYCRNPDGSDSERPWCTTDNVERFCDLRSCGPNLPPVKGSKSQR 283

Qy 171 -SSRPTCYLIGKGAKYKGITSITSGIQCWNNSPIHE---HSYRGKDLRENNYCRNPRGE 174
 Db 284 RNKSKALNCFRGKGDYRGTNTTSAGYPCQRMDAQSPHOHRFVPEKYACKCOLRENFCRN 229

Qy 230 PDGGRAPHCTTNSQVRMYC-KIPSC 255
 Db 344 PDGSEAPWCFTSRPGLRHFQHCPICR 370

RESULT 15

S00657 apoprotein(a) (EC 3.4.21.-) precursor [validated] - human
 N;Alternate names: apolipoprotein(a); lipoprotein(a); chain apo(a)
 C;Species: Homo sapiens (man)
 C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
 C;Accession: S00657; A28017; R47277; 16096; A47233; 157415; 165266
 R;McLean, J.W.; Tomlinson, J.E.; Kuang, W.J.; Eaton, D.L.; Chen, E.Y.; Fless, G.M.; Scar
 Nature 330, 132-137, 1987
 A;Title: cDNA sequence of human apolipoprotein(a) is homologous to plasminogen.
 A;Reference number: S00657; MUID:88039107; PMID:3670400
 A;Accession: S00657
 A;Molecule type: mRNA
 A;Residues: 1-4548 <MOL>
 A;Cross-references: UniProt:POB519; GB:X06290; EMBL:X06696; NID:928619; PIDN:CAA29618_1;
 R;Fenton, D.L.; Fless, G.M.; Kohr, W.J.; McLean, J.W.; Xu, Q.T.; Miller, C.G.; Lawn, R.M.
 Proc. Natl. Acad. Sci. U.S.A. 84, 3224-3228, 1987
 A;Reference number: A28017; MUID:87204109; PMID:3472206
 A;Accession: A28017
 A;Molecule type: protein
 A;Residues: 20-21, P, 23-34, 177-179, 'N', 181-186, 'T', 188-196, 'DKG', 200-292-314, 'W', 316-31
 X, 4396-4401 <ENT>
 R;Nade, D.P.; Clarke, J.G.; Lindahl, G.E.; Liu, A.C.; Zysow, B.R.; Meier, K.; Schwartz, R
 proc. Natl. Acad. Sci. U.S.A. 90, 1369-1373, 1993

A;Title: 5' control regions of the apolipoprotein(a) gene and members of the related plasmalogens
A;Reference number: A47277; MUID:91165698; PMID:7679504
A;Accession: A47277
A;Status: preliminary; translation not shown; translated from GB/EMBL/DDJB
A;Molecule type: DNA
A;Residues: 1-16 <RES>
A;Cross-references: GB:L07899; NID:996973; PID:9267974
R;Magaretti, N.; Acquati, F.; Magagni, P.; Bruno, L.; Pontoglio, M.; Rocchi, M.; Sacco, Proc. Natl. Acad. Sci. U.S.A. 89, 11584-11588, 1992
A;Title: Characterization by yeast artificial chromosome cloning of the linked apolipoprotein(a) gene
A;Accession: A47233; MUID:93087573; PMID:1454851
A;Accession: I60906
A;Status: preliminary; translated from GB/EMBL/DDJB
A;Molecule type: DNA
A;Residues: 1-16 <RES>
A;Cross-references: GB:M90078; NID:9178786; PID:AAA35547.1; PID:9553188
A;Accession: A47233
A;Status: preliminary; translation not shown; translated from GB/EMBL/DDJB
A;Residues: 1-16 <RES>
A;Cross-references: GB:M90079; NID:9178784; PID:AAA35546.1; PID:9553187
A;Ichinoze, A.
Biochemistry 31, 3113-3118, 1992
A;Title: Multiple members of the plasminogen-apolipoprotein(a) gene family associated with reference number: 152415; MUID:92207924; PMID:1554698
A;Accession: I62415
A;Status: preliminary; translated from GB/EMBL/DDJB
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A;Note: apo(a) gene 1 (nomenclature of reference 152415)
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A;Gene: GDB:LPA
A;Cross-references: GDB:1120699; OMIM:152200
A;Note: several genes closely linked on chromosome 6 are identical in the first coding exons or kringle repeats
C;Superfamily: apolipoprotein(a); kringle homology; trypsin homology/
C;Keywords: hydrolase; kringle; lipid binding; lipoprotein; serine proteinase
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F;256-333/Domain: kringle homology <KR3>
F;370-47/Domain: kringle homology <KR4>
F;84-561/Domain: kringle homology <KR5>
F;598-675/Domain: kringle homology <KR6>
F;712-789/Domain: kringle homology <KR7>
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F;40-1017/Domain: kringle homology <KR9>
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F;168-1245/Domain: kringle homology <KR11>
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Best Local Similarity 41.2%; Pred. No. 3.3e-46; Matches 81; Mismatches 58; Gaps 5;
Matches 129; Conservative 45; Indels 58; Gaps 5;
A;Y 3 LSCKCTGAGKNGTGTMSKTRGKTCWWSSTSPHRPRSPATHPSGELLENYCRNPNDP 62
D; 3779 VODCYHGDQSYRGFSFTVTRGTCQWSMSMPHWRQRTTEYVPGNGLTRNYCRNPDAE 3838
Q; Y 63 QGWMCYTDPKRYDQDILEE-----ECM 89
D; b 3839 R-PWCYMDPSYRMEYCILQCPVMSLITLPTVPUVPSLSPBAPTEINSTGYC 3897
Q; Y 90 HCSGENYCKISKTMGSGECAWDSDSOPHSRANGYIPSKEPNPKNLKQYCRNPDRRELPCWCF 149
D; b 3958 TMPSVRWYCNLTRCPVTESSVLTTPTVAWPVSTEAEPOCRPEKSPVVQDCHGDRS 4017
Q; Y 186 YRGNAVAVTWSGHTQHNSAQTHTRPENPKNDLBNYCRNPDGKRAWMCHTNSQV 245
D; b 4018 YRISSTTVTGTCQSHSMSMIPHHQRTPENVPNAGLIENTYCRNPDSGKQPMCYTDPGV 4077
Q; Y 246 RWYCKLPSCDSS 258
D; b 4078 RWYCNLTCQSET 4090

Search completed: July 27, 2005, 03:30:30
Job time : 17 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: July 27, 2005, 03:21:14 ; Search time 61 Seconds
(without alignment)
2182.633 Million cell updates/sec

Title: US-09-502-176-2
Perfect score: 1540

Sequence: 1 VYLSBCKTGKNYRGTM SK..... TNSQVRWEYCKIRSCDSSPV 260

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1535	99.7	810	1 PLMN_HUMAN
2	1442	93.6	810	1 PLMN_MACMU
3	1306	84.8	359	2 Q8MRL1
4	1299	84.4	812	1 PLMN_RAT
5	1292	83.9	790	1 PLMN_PIG
6	1291	83.8	812	1 PLMN_BOVIN
7	1279	83.1	466	2 Q6TCI0
8	1279	83.1	812	1 PLMN_MOUSE
9	1237	80.3	810	1 PLMN_ERTEU
10	1203.5	78.1	759	2 Q7TP84
11	1160	75.3	806	1 PLMN_MACEU
12	996	64.7	818	1 PLPB6
13	881	57.2	2869	2 Q28398
14	809.5	52.6	449	2 Q6GP14
15	809.5	52.6	716	2 Q91691
16	797	51.8	728	1 HGF_HUMAN
17	796	51.7	709	2 Q7ZPN9
18	795.5	51.7	717	2 P70005
19	782	50.8	728	1 HGF_RAT
20	778	50.5	726	2 Q90978
21	778	50.5	730	2 Q867B7
22	777	50.5	728	2 Q8C9G5
23	776.5	50.4	710	2 Q91402
24	776	50.4	728	1 HGF_MOUSE
25	774	50.3	730	2 Q768S1
26	772	50.1	704	2 Q90865
27	772	50.1	728	2 Q9BHQ9
28	766.5	49.8	709	2 Q902N6
29	766.5	49.8	716	2 P70521
30	764.5	49.0	405	2 Q788Q2
31	753.5	48.9	716	1 HGFL_MOUSE

RESULT 1	PRT; 810 AA.
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AC: P00747; Q15146; Q6PA00;	
DT: 21-JUL-1986 (Rel. 0); Created)	
DT: 01-MAR-1989 (Rel. 10); Last sequence update)	
DT: 25-OCT-2004 (Rel. 45); Last annotation update)	
DE: Plasminogen precursor (EC 3.4.21.7) [contains: Angiotatin1].	
GN: Name=PLUG;	
OS: Homo sapiens (Human)	
OC: Bucephala; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC: Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX: NCBI_TAXID=9606;	
RN: [1]	
RP: SEQUENCE FROM N.A., AND VARIANT ASN-472.	
RX: MEDLINE=90202879; PubMed=2318848;	
RA: Petersen T.E., Marzen M.R., Ichinose A., Davie B.W.;	
RR: "Characterization of the gene for human plasminogen, a key proenzyme in the fibrinolytic system";	
RT: J. Biol. Chem. 265:6104-6111(1990).	
RN: [2]	
RP: SEQUENCE FROM N.A.	
RX: MEDLINE=87162490; PubMed=3030813; DOI=10.1016/0014-5793(87)81001-6;	
RA: Forssgren M., Raden C.G., Dodd I., Carey J.E., Lawrence G.M.P.,	
RA: Blowne M.J., Chapman C.G., Dodd I., Carey J.E., Lawrence G.M.P.,	
RA: Mitchell D., Robinson J.H.,	
RT: "Molecular cloning and characterization of a full-length cDNA clone for human plasminogen.";	
FEBS Lett. 213:254-260(1987).	
RN: [3]	
RP: SEQUENCE FROM N.A.	
RX: MEDLINE=87162490; PubMed=3030813; DOI=10.1016/0014-5793(87)81001-6;	
RA: Forssgren M., Raden C.G., Dodd I., Carey J.E., Lawrence G.M.P.,	
RA: Mitchell D., Robinson J.H.,	
RT: "Expression of recombinant human plasminogen and aglycoplasminogen in HeLa cells,"	
RT: Submitted (Oct-1991) to the EMBL/GenBank/DBJ databases.	
RN: [4]	
RP: SEQUENCE FROM N.A., AND VARIANTS LYS-57; GLN-133; HIS-261; TRP-408;	
RP: ASN-472; VAL-494 AND TRP-523.	
RA: Rieder J.J., Armel T.Z., Carrington D.P., Ozuna M., Kuldanek S.A.,	
RA: Rajkumar N., Totis E.J., Yi Q., Nickerson D.A.;	
RT: "SeartleinPs. NHLBI Hu6682 program for genomic applications, UW-RT: FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu)";	
RT: Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.	
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RX: MEDLINE=22388257; PubMed=1247932; DOI=10.1073/pnas.242603899;	
RA: Strasserberg R.L., Feinbold R., Grouse L.H., Derge J.G.,	
RA: Klausner R.D., Collins S.S., Wagner L., Shemesh C.M., Schuler G.D.,	
RA: Alischul S.F., Zeeberg B., Buetow K.H., Schaeffer C.F., Bhat N.K.,	
RA: Hopkins R.S., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,	
RA: Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong J.,	
RA: Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,	
RA: Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,	

RA Raha S.S., Loquillard N.A., Peters G.J., Abramson R.D., Mulahay S.J., Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Guarante P.H., Rodriguez S., McEwan P.J., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Soedergran E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Buffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalius D.E., Schnarch A., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

[6] SEQUENCE OF 20-810, AND VARIANT ASN-472; R.P. Sottrup-Jensen L., Petersen T.E., Magnusson S.; Submitted (JUL-1977) to the PIR data bank.

[7] SEQUENCE OF 292-810 FROM N.A. MEDLINE=85023311; PubMed=614861;

RX RA Malinowski D.P., Sadler J.E., Davie E.W.; "Characterization of a complementary deoxyribonucleic acid coding for human and bovine plasminogen.;" Biochemistry 23:4243-4250(1984).

RN [8] R.P. SEQUENCE OF 20-100; R.P. MEDLINE=509329; PubMed=122932;

RX RA Wiman B., Wallen P.; "Structural relationship between 'glutamic acid' and 'lysine' forms of human plasminogen and their interaction with the NH₂-terminal activation peptide as studied by affinity chromatography.;" Eur. J. Biochem. 50:489-494(1975).

[9] R.P. SEQUENCE OF 95-580: 581-626; 657-700 AND 732-810, AND VARIANT ASN-472. R.A. Sottrup-Jensen L., Claeyns H., Zaidel M., Petersen T.E., Magnusson S.; (In) Davidson J.F., Rowan R.M., Samama M.M., Desnoyers P.C. (eds.); R.L. Raven Press, New York (1978).

RN [10] R.P. SEQUENCE OF 483-604. RX MEDLINE=76043692; PubMed=126863;

RX RA Wiman B., Wallen P.; "Amino-acid sequence of the cyanogen-bromide fragment from human plasminogen that forms the linkage between the plasmin chains.;" Eur. J. Biochem. 58:539-547(1975).

RN [11] R.P. SEQUENCE OF 581-810. RX MEDLINE=77225245; PubMed=142009;

RX RA Wiman B.; "Primary structure of the B-chain of human plasmin.;" R.T. Bur. J. Biochem. 76:129-137(1977).

R.L. [12] R.P. ACTIVE SITE. RX MEDLINE=7314248; PubMed=4634729;

R.A. Robbins K.C., Bernabe P., Arzadon L., Summaria L.; "The primary structure of human Plasminogen. II. The histidine loop of human plasmin: light (B) chain active center histidine sequence.;" R.N. [13] J. Biol. Chem. 248:1631-1633(1973).

R.P. ACTIVE SITE. RX MEDLINE=69224739; PubMed=4240117;

R.A. Grosskopf W.R., Summaria L., Robbins K.C.; "Studies on the active center of human plasmin. Partial amino acid sequence of a peptide containing the active center serine residue.;" R.L. J. Biol. Chem. 244:3550-3559(1969).

RN [14] R.P. OMEGA-AMINOCARBOXYLIC ACID-BINDING SITES. RX MEDLINE=82213905; PubMed=619539;

R.A. Trexler M., Vail Z., Patthy L.; "Structure of the omega-aminocarboxylic acid-binding sites of human plasminogen. Arginine 70 and aspartic acid 56 are essential for binding of ligand by kringle 4.;" R.L. J. Biol. Chem. 257:7401-7406(1982).

RN [15] FIBRIN AND OMEGA-AMINOCARBOXYLIC ACID BINDING SITES. R.P. MEDLINE=85054794; PubMed=6094526;

RX RA Vali Z., Patthy L.; "The fibrin-binding site of human plasminogen. Arginines 32 and 34 are essential for fibrin affinity of the kringle 1 domain.;" J. Biol. Chem. 259:13690-13694(1984).

RN [16] PHOSPHORYLATION SITE SER-597. RX MEDLINE=97345939; PubMed=2201958; DOI=10.1021/bi970328d;

RX RA Wang H., Prorok M., Bretthauer R.K., Castellino F.J.; "Serine-578 is a major phosphorylation locus in human plasma plasminogen.;" Biochemistry 36:8100-8106(1997).

RN [17] CARBOHYDRATE-LINKAGE SITES. RX MEDLINE=88185322; PubMed=3356193;

RX RA Marti T., Schaller J., Rock E.B., Schmid K., Kamerling J.P., Gerwig G.J., van Halbeek H., Vliegenthart J.F.; "The N- and O-linked carbohydrate chains of human, bovine and porcine plasminogen. Species specificity in relation to sialylation and fucosylation patterns.;" Eur. J. Biochem. 173:57-63(1988).

RN [18] CARBOHYDRATE-LINKAGE SITE SER-268. RX MEDLINE=97207306; PubMed=905441; DOI=10.1074/jbc.272.11.7408;

RX RA Pirie-Shepherd S.R., Stevens R.D., Andon N.L., Englund J.J., Pizzo S.V.; "Evidence for a novel O-linked sialylated trisaccharide on Ser-248 of human plasminogen 2.;" J. Biol. Chem. 272:7408-7411(1997).

RN [19] CHARACTERIZATION OF ANGIOSTATIN, AND PARTIAL SEQUENCE. RX MEDLINE=95042726; PubMed=7525077; DOI=10.1016/0022-8644(94)90200-3;

RX RA O'Reilly M.S., Holmren L., Shing Y., Chen C., Rosenthal R.A., Moses M., Lane W.S., Cao Y., Sage E.H., Folkman J.; "Angiostatin: a novel angiogenesis inhibitor that mediates the suppression of metastases by a Lewis lung carcinoma.;" R.L. Cell 79:315-328(1994).

RN [20] CHARACTERIZATION OF ANGIOSTATIN. RX MEDLINE=97238710; PubMed=910221;

RX RA Sim B.K., O'Reilly M.S., Liang H., Fortier A.H., He W., Madsen J.W., Lapcevich R., Nancy C.A.; "A recombinant human angiostatin protein inhibits experimental primary and metastatic cancer.;" Cancer Res. 57:1329-1334(1997).

RN [21] X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 374-461. RX MEDLINE=92031502; PubMed=1657148;

RX RA Mulchak A.M., Tulinsky A., Ravichandran K.G.; "Crystal and molecular structure of human plasminogen kringle 4 refined at 1.9-A resolution.;" R.L. Biochemistry 30:10576-10588(1991).

RN [22] X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF 374-461. RX MEDLINE=92031503; PubMed=1657149;

RX RA Wu T.-P., Padmanabhan K., Tulinsky A., Mulchak A.M.; "The refined structure of the epsilon-aminocaproic acid complex of human plasminogen kringle 4.;" Biochemistry 30:10589-10594(1991).

RN [23] X-RAY CRYSTALLOGRAPHY (1.67 ANGSTROMS) OF 376-454. RX PubMed=1529955;

RX RA Stoe B., Yamano A., Whitlow M., Teeter M.M.; "Structure of human plasminogen kringle 4 at 1.68 Angstrom and 277 K. A possible structural role of disordered residues.;" Acta Crystallogr. D 53:169-178(1997).

RX X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 102-181. RX MEDLINE=96180581; PubMed=8611560; DOI=10.1021/bi9521351;

RX RA Mathews I.I., Vandenhoff-Hanaver P., Castellino F.J., Tulinsky A.; "Crystal structures of the recombinant kringle 1 domain of human

FT DISULFID 296 335 By similarity.
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 FT DISULFID 377 454 By similarity.
 FT DISULFID 398 437 By similarity.
 FT DISULFID 426 449 By similarity.
 FT DISULFID 481 560 By similarity.
 FT DISULFID 502 543 By similarity.
 FT DISULFID 531 555 By similarity.
 FT DISULFID 567 685 Interchain (By similarity).
 FT DISULFID 577 585 Intercain (By similarity).
 FT DISULFID 607 623 By similarity.
 FT DISULFID 699 766 By similarity.
 FT DISULFID 729 745 By similarity.
 FT DISULFID 756 784 O-linked (GalNAc...) (By similarity).
 FT CARBOHYD 365 365 SEQUENCE 810 AA; 90255 MW; A75E1C51A1A0F24A CRC64;

Query Match 93.6%; Score 1442; DB 1; Length 810;
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Qy 1 VVLSBCKTGNGKNGYRGTMSKTKNGITCKWKSSTSPHRFRSPATHSGLEENYCRNPDN 60
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 Db 218 GYIPSKFPNKLNKKNYCRNPDRDLRPWCFPTDNPKRMLCDIPRCTTPPPSGPTYCLK 277

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 Db 278 GTGENYGRNVAVTWSGHTCQWQAQTPTHTPENPKQDENCYCRNPGKPRWCWT 337

Qy 241 TNSQVRKEYCKLPSCDSSPV 260
 Db 338 TNSQVRKEYCKLPSCDSSPV 357

RESULT 3
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AC Q8WMR1; DT 01-MAR-2002 (T-EMBLel. 20, Created)
 DT 01-MAR-2002 (T-EMBLel. 20, last sequence update)
 DE Plasminogen (Fragment).
 OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis. NCBI_TaxID=9615; NCBI_TaxID=1016; RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Bangert K., Johnsen A.H., Thorsen S.;
 RT "rat plasminogen, cDNA and gene structure";
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
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 RC TISSUE=Liver;
 RX MEDLINE=91250378; PubMed=1645711;
 RA Kanalas J.J., Marker S.P.;
 RT "Identification of the rat Heymann nephritis autoantigen (GP330) as a receptor site for plasminogen.";
 RL J. Biol. Chem. 266:10825-10829(1991).

CC -1- FUNCTION: Plasmin dissolves the fibrin of blood clots and acts as a proteolytic factor in a variety of other processes including embryonic development, tissue remodeling, tumor invasion, and inflammation; in ovulation it weakens the walls of the Graafian follicle. It activates the urokinase-type plasminogen activator, collagenases and several complement zymogens, such as C1 and C5.

CC -1- FUNCTION: Angiostatin is an angiogenesis inhibitor that blocks neovascularization and growth of experimental primary and metastatic tumors in vivo (By similarity).

CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Iys-|Xaa > Arg-|Xaa; higher selectivity than trypsin. Converts fibrin into soluble products.

CC -1- ENZYME REGULATION: Converted into plasmin by plasminogen activators, both plasminogen and its activator being bound to fibrin. Cannot be activated with streptokinase.

CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- MISCCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin
 CC immediately after dissociation from the clot.
 CC -!- MISCCELLANEOUS: In the presence of the inhibitor, the activation
 CC involves only cleavage after Arg-581, resulting in 2 chains held
 CC together by 2 disulfide bonds. Without the inhibitor, the
 CC activation involves also removal of the activation peptide (By
 CC similarity).
 CC -!- SIMILARITY: Belongs to the peptidase S1 family. Plasminogen
 CC subfamily.
 CC -!- SIMILARITY: Contains 5 kringle domains.
 CC -!- SIMILARITY: Contains 1 PNA domain.

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EMBL; AJ242649; CAB46014.1; -.
 DR EMBL; M62832; AA041884.1; -.
 DR PIR; A40522; A40522.
 DR HSSP; P00747; 1PMK.
 DR MEROPS; S01; 233; -.
 RGD; 619893; Plg.
 DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR000014; PAN.
 DR InterPro; IPR000014; Peptidase_S1.
 DR InterPro; IPR00134; Peptidase_S1A.
 DR InterPro; IPR00366; Peptidase_S1A_PR.
 DR InterPro; IPR011358; Pept_SIA_Plasm.
 DR InterPro; IPR00503; Pept_Ser_Cys.
 DR Pfam; PF00051; Kringle_5.
 DR Pfam; PF00054; PAN; 1.
 DR Pfam; PF00089; TRYPSIN; 1.
 DR SMART; SMM00473; PAN_AP; 1.
 DR SMART; SMM0020; TTP_SPC; 1.
 PROSITE; PS00021; KRINGLE_1; 5.
 PROSITE; PS00070; KRINGLE_2; 5.
 PROSITE; PS00948; PAN; 1.
 PROSITE; PS00240; TRYPSIN_DOM; 1.
 PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS0015; TRIPSIN_SER; 1.
 KW Blood coagulation; Fibriolysis; Glycoprotein; Hydrolase; Kringle;
 KW Plasma; Repeat; Serine protease; Signal; Tissue remodeling; Zymogen.
 FT SIGNAL 1 19 By similarity.
 FT CHAIN 20 812 By similarity.
 FT PEPTIDE 20 581 Plasmin heavy chain A.
 FT CHAIN 98 581 Activation Peptide (By similarity).
 FT CHAIN 98 ?436 Plasmin short form of chain A.
 FT CHAIN 582 812 Angiotatin.
 FT DOMAIN 20 98 Plasmin light chain B.
 FT DOMAIN 102 181 Kringle 1.
 FT DOMAIN 184 262 Kringle 2.
 FT DOMAIN 274 352 Kringle 3.
 FT DOMAIN 375 454 Kringle 4.
 FT DOMAIN 580 812 Kringle 5.
 FT DOMAIN 582 812 Serine protease.
 FT ACT_SITE 624 624 Charge relay system (By similarity).
 FT ACT_SITE 667 667 Charge relay system (By similarity).
 FT ACT_SITE 762 762 Charge relay system (By similarity).
 FT DISULFID 49 73 By similarity.
 FT DISULFID 53 61 By similarity.
 FT DISULFID 103 181 By similarity.

FT DISULFID 124 164 By similarity.
 FT DISULFID 152 176 By similarity.
 FT DISULFID 185 262 By similarity.
 FT DISULFID 188 316 By similarity.
 FT DISULFID 206 245 By similarity.
 FT DISULFID 234 257 By similarity.
 FT DISULFID 275 352 By similarity.
 FT DISULFID 296 335 By similarity.
 FT DISULFID 324 347 By similarity.
 FT DISULFID 376 454 By similarity.
 FT DISULFID 397 437 By similarity.
 FT DISULFID 425 449 By similarity.
 FT DISULFID 481 560 By similarity.
 FT DISULFID 502 543 By similarity.
 FT DISULFID 531 555 By similarity.
 FT DISULFID 568 687 Interchain (By similarity).
 FT DISULFID 578 586 By similarity.
 FT DISULFID 609 625 By similarity.
 FT DISULFID 701 768 By similarity.
 FT DISULFID 731 747 By similarity.
 FT DISULFID 758 786 By similarity.
 FT CONFFLICT 418 418 A -> S (in Ref. 2).
 SQ SEQUENCE 812 AA; 90535 MW; 8C703C51410BRC9E CRC64;
 Query Match 84.4%; Score 1299; DB 1; Length 812;
 Best Local Similarity 82.6%; Pred. No. 1e-90; Gaps 0;
 Matches 213; Conservative 21; Mismatches 24; Indels 0; Gaps 0;

Qy 1 VYLSCCKTGKANGTGTMSKTKQKSSTSPPHRPRSPATHPSGLEBNENCRNPDN 60
 Db 98 VYLSCCKTGKANGTGTMSKTKQKSSTSPPHRPRSPATHPSGLEBNENCRNPDN 60
 Qy 61 DPQGWCYTDPERKYDQDILECEBECMCSGENYDGKISKTMMSGLECOAWQSOPRAH 120
 Db 158 DEQGWCVTDPDQRVYECNCIPECEBECMCSGEKVBKISKTMMSGLECOAWQSOPRAH 217
 Qy 121 GYIPSKFPNPKNLKQYCRRPDRLEPFWCFPTDNKRWLCDIPRCTTTPPSGPTYQCLK 180
 Db 218 GYIPAKFPNSKLKOMYCRNPDGEEPRPWFPTDNPKRWEYCDIPRCTTTPPPGPTYQCLK 277
 Qy 181 GTGEGYRGWAVTSGHTQHWSAQTOPKTHERTPENPKLNLDNYCNPDKGRAPWCHT 240
 Db 278 GRGENYGRGVSVTAGKTCORWSBOTPRHRNTPENPKLNLENTYCNPDKGRAPWCHT 337
 Qy 241 TNSQVRWVEYKIPSDSS 258
 Db 338 TDSDQWRWECRIPSGGS 355

RESULT 5
 BLMN_PIG ID_PLMN_PIG STANDARD; PRT; 790 AA.
 AC P06687; DT 01-JAN-1988 (Rel. 06, Created)
 AC P06687; DT 01-FEB-1991 (Rel. 17, Last sequence update)
 AC P06687; DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DB Plasminogen (EC 3.4.21.7).
 GN Name=PIG;
 OS Sub arcota (PIg).
 OC Bivalvia; Monotaxis; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sub.
 NCBI_TaxID=9823; [1]
 RN SEQUENCE OF 1-560.
 RN Schaller J., Marti T., Roesslelet S.J., Kaempfer U., Rickli E.B.;
 RN "Amino acid sequence of the heavy chain of porcine plasmin. Comparison
 RN of the carbohydrate attachment sites with the human and bovine
 RN species"; Fibrinolysis 1:91-102 (1987).
 RN [2]
 RN SEQUENCE OF 450-730.
 RX MEDLINE:85203907; PubMed:3146533;
 RX Marti T., Schaller J., Rickli E.B.;

RT "Determination of the complete amino-acid sequence of porcine
 RT miniplasminogen."
 RL Bur. J. Biochem. 149:279-285 (1985).
 RN [3]
 RP CARBOHYDRATE-LINKAGE SITES.
 RX MEDLINE=88185329; PubMed=3356193;
 RA Marti T., Schaller J., Rickli H.E., Schmid K., Kammerling J.P.,
 RA Gerwig G.J., van Halbeek H., Vliegenthart J.P.;
 RT "The N- and O-linked carbohydrate chains of human, bovine and porcine
 RT plasminogen. Species specificity in relation to sialylation and
 RT fucosylation patterns".
 RL Bur. J. Biochem. 175:57-63 (1988).
 CC -!
 CC FUNCTION: Plasmin dissolves the fibrin of blood clots and acts as
 CC a proteolytic factor in a variety of other processes including
 CC embryonic development, tissue remodeling, tumor invasion, and
 CC inflammation; in ovulation it weakens the walls of the Graafian
 CC follicle. It activates the urokinase-type plasminogen activator,
 CC collagenases and several complement zymogens, such as C1 and C5.
 CC It cleaves fibrin, fibronectin, thrombospondin, laminin and von
 CC Willerstrand factor.
 CC -!
 CC CATALYTIC ACTIVITY: Preferential cleavage: Lys-|-Xaa > Arg-|-Xaa;
 CC higher selectivity than trypsin. Converts fibrin into soluble
 CC products.
 CC -!
 CC ENZYME REGULATION: Converted into plasmin by Plasminogen
 CC activators, both plasminogen and its activator being bound to
 CC fibrin. Cannot be activated with streptokinase.
 CC -!
 CC SUBCELLULAR LOCATION: Secreted.
 CC -!
 CC PTM: N-linked glycan contains N-acetylglactosamine, sialic acid and
 CC is core fucosylated. O-linked glycans consist of Gal-GalNAc
 CC disaccharide which is modified with up to 2 sialic acid residues
 CC (microheterogeneity).
 CC -!
 CC MISCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin
 CC immediately after dissociation from the clot.
 CC -!
 CC SIMILARITY: Belongs to the peptidase_S1 family. Plasminogen
 CC subfamily.
 CC -!
 CC SIMILARITY: Contains 5 kringle domains.
 CC
 DR PIR: S03733; PLPG
 DR HSSP: P00747; IBUI.
 DR MEROPS: S01.233; -.
 DR GlycosuiredB; P06867; -.
 DR InterPro; IPR00001; Kringle.
 DR InterPro; IPR00301; PAN.
 DR InterPro; IPR00360; Pan.app
 DR InterPro; IPR00125; Peptidase_S1.
 DR InterPro; IPR00134; Peptidase_SIA.
 DR InterPro; IPR00366; Peptidase_SIA_pr.
 DR InterPro; IPR00903; Pept_Ser_Cys.
 DR Pfam; PF00051; Kringle_5.
 DR Pfam; PF00024; PAN_1.
 DR Pfam; PF00089; TRYPSIN; 1.
 DR Pfam; PF0001150; Plasmin; 1..
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00018; KRINGLE.
 DR PRINTS; PR0105; PROTHROMBIN.
 DR SMART; SNO130; Kr_5.
 DR SMART; SNO0473; PAN_AP; 1.
 DR SMART; SNO0020; TRYSP_SPC; 1.
 DR PROSITE; PS00021; KRINGLE_1; 5.
 DR PROSITE; PS00070; KRINGLE_2; 5.
 DR PROSITE; PS000395; Kringle_5.
 DR SMART; SNO130; Kr_5.
 DR SMART; SNO0473; PAN_AP; 1.
 DR PROSITE; PS00024; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; FALSE_NEG.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Blood coagulation; Direct protein sequencing; Fibrinolysis;
 KW Tissue remodeling; Zymogen.
 FT CHAIN 1 560 Plasmin heavy chain A.
 FT CHAIN 561 790 Plasmin light chain B.
 FT DOMAIN 1 79 Plasmin.
 FT DOMAIN 561 790 Serine protease.
 FT DOMAIN 84 162 Kringle 1.

RESULT 6
 PIRN_BOVIN
 ID PIRN_BOVIN STANDARD; PRT; 812 AA.
 AC P06868; Q28162;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DE Plasminogen precursor (EC 3.4.21.7).
 DE Name=PIG;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bos.
 NCBI_TAXID=9913;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC TISSUE-Liver;
 RA Berglund L., Andersen M.D., Petersen T.B.;
 RA "Cloning and characterization of the bovine plasminogen cDNA.",
 RL Int. Dairy J. 5:593-603(1995).
 RN [2]
 RP SEQUENCE OF 27-812, AND CARBOHYDRATE-LINKAGE SITES.
 RK MEDLINE=85203905; PubMed=3846532;
 RA Schaller J., Moser P.W., Dannegger-Muller G.A.K., Rosselet S.J.,
 RA Kampfer U., Rickli H.E.;
 RT "Complete amino acid sequence of bovine plasminogen. Comparison with
 RT human Plasminogen.",
 RL Bur. J. Biochem. 149:267-278 (1985).
 RN [3]
 RP SEQUENCE OF 706-812 FROM N.A.
 RK MEDLINE=85023311; PubMed=6148961;
 RA Malinowski D.P., Sadler J.E., Davie E.W.;
 RT "Characterization of a complementary deoxyribonucleic acid coding for
 RT human and bovine plasminogen.",
 RL Biochemistry 23:4243-4250(1984).

DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR003014; PAN.
 DR InterPro; IPR003609; Pan app.
 DR InterPro; IPR003966; Peptidase_S1A_pr:
 DR InterPro; IPR001400; Somatotropin.
 DR Pfam; PF00051; Kringle; 4.
 DR Pfam; PF00024; PAN; 1.
 DR Prints; PR00019; KRINGLE.
 DR Prints; PR01505; PROTHROMBIN.
 DR Prodom; PR00059; Kringle; 4.
 DR SMART; SM00130; KR; 4.
 DR SMART; SM00473; PAN_AP; 1.
 DR PROSITE; PS00021; KRINGLE_1; 4.
 DR PROSITE; PS50070; KRINGLE_2; 4.
 DR PROSITE; PS50948; PAN; 1.
 DR PROSITE; PS00338; SOMATOTROPIN_2; UNKNOWN_1.
 SQ SEQUENCE 466 AA; 52717 MW; 3ED3298C34C39116 CRC64;
 Query Match 83.1%; Score 1279; DB 2; Length 466;
 Best Local Similarity 81.0%; Pred. No. 1.9e-89;
 Matches 209; Conservative 22; Mismatches 27; Indels 0; Gaps 0;
 QY 1 VLYSECKTGKNGNYRGTMSKTKNGTICRKNSSTSRRPRISSPATHPSEGLEN
 98 VYLSECKTGKNGNYRGTMSKTKNGTICRKNSSTSRRPRISSPATHPSEGLEN CRNPDN 60
 QY 61 DPOQGWCYTDPKEKRYDQLECEBECMECSEGEMDGKISKTMGLEQAMWSOPRAH 120
 Db 158 DEQGPWCYTDPKEKRYDQLECEBECMECSEGEMDGKISKTMGLEQAMWSOPRAH 217
 QY 121 GYIPSKFPNKLQKKNYCRNDFRLRPWCFTDPNKGELDIPRCTTPPSGGTYQCLK 180
 218 GYIPAKFPKPSKLQKKNYCRNDFRLRPWCFTDPKRWEDIPRCTTPPSGGTYQCLK 277
 QY 181 GTGENVRGNATVWASHTCOWHSQAQPTPHTRTPENFPCQNDENYCRNDFGRKAPWCH 240
 278 GRRGENVRGTWASHTCOWHSQAQPTPHTRTPENFPCQNDENYCRNDFGRKAPWCH 337
 QY 241 TNSQYRWEYCRPSDSS 258
 Db 338 TDSDQRWEYCEIPSGESS 355

RESULT 8

PLMN_MOUSE STANDARD; PRT; 812 AA.

ID P20918; OCIS2; Q9WJ5; DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Plasminogen precursor (EC 3.4.21.7) [Contains: Angiotatin].
 GN Name=Plg; OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. OC NCBI_TaxId=10900; [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:9118812; PubMed=2091600;
 RT "Characterization of the cDNA coding for mouse plasminogen and localization of the gene to mouse chromosome 17.";
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/Sv;
 RA Brathwaite M., Waeztz P., Qian Y., Dudekula D., Schlessinger D., Nagaija R.;
 RT "Genomic sequence analysis in the mouse t-complex region.";
 RL submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.

RC TISSUE=Liver;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Sheehan C.M., Schuler G.D., Altschul S.F., Zeeberg B., Bustow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heile F., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Munizy D.M., Sodergren E.J., Lu X., Gibbs R.A., Farley J., Helton E., Kettman M., Madden A., Rodriguez S., Sanchez A., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalius D.E., Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.; RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [4]
 RP SEQUENCE OF 1-16 FROM N.A.
 RC STRAIN=129/SvJ; TISSUE=Liver;
 RN PubMed=12149246; DOI=10.1074/jbc.M202502200;
 RA Bachanach A., Gutierrez A., Fowler B.J., Bugge T.H., Degen J.L., Farmer R.J., Miles L.A.; RT "Localization of regulatory elements mediating constitutive and cytokine-stimulated plasminogen gene expression";
 RL J. Biol. Chem. 277:38579-38588 (2002).
 RN [5]
 RP CHARACTERIZATION OF ANGIOSTATIN AND PARTIAL SEQUENCE.
 RX MEDLINE=954228; PubMed=7525077; DOI=10.1016/0022-8674(94)90200-3;
 RA O'Reilly M.S., Holmren L., Shing Y., Chen C., Rosenthal R.A., Moses M., Lane W.S., Cao Y., Sage E.H., Folkman J.;
 RT "Angiotatin: a novel angiogenesis inhibitor that mediates the suppression of metastases by a Lewis lung carcinoma.";
 RL Cell 79:315-328 (1994).
 CC -- FUNCTION: Plasmin dissolves the fibrin of blood clots and acts as a proteolytic factor in a variety of other processes including embryonic development, tissue remodeling, tumor invasion, and inflammation; in ovulation it weakens the walls of the Graafian follicle. It activates the urokinase-type plasminogen activator, collagenases and several complement zymogens, such as C1 and C5. It cleaves fibrin, fibronectin, thrombospondin, laminin and von Willebrand factor.
 CC -- FUNCTION: Angiotatin is an angiogenesis inhibitor that blocks neovascularization and growth of experimental primary and metastatic tumors *in vivo*.
 CC -- FUNCTION: Plasminogen: preferential cleavage: Lys-| -xaa > Arg-| -xaa; higher selectivity than trypsin. Converts fibrin into soluble products.
 CC -- ENZYME REGULATION: Converted into Plasmin by plasminogen activators, both plasminogen and its activator being bound to fibrin. Cannot be activated with streptokinase.
 CC -- SUBCELLULAR LOCATION: Secreted.
 CC -- MISCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin immediately after dissociation from the clot.
 CC -- MISCELLANEOUS: In the presence of the inhibitor, the activation involves only cleavage after Arg-581, resulting in 2 chains held together by 2 disulfide bonds. Without the inhibitor, the activation involves also removal of the activation peptide.
 CC -- SIMILARITY: Belongs to the peptidase S1 family. Plasminogen subfamily.
 CC -- SIMILARITY: Contains 5 kringle domains.
 CC --
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Qy	1	VYLLBACKTGNGKNTGTMKNGTCKOMNSSPHRPRSPATHPSGCLEBNYCNRNND	DR	InterPro; IPR01358; Pept_SIA_Plasm
Ov	167	-----TPPSSGGPTYQCLKGTCGYRGNVAVTWSGHCOHMSAQTPTHF 211	DR	InterPro; IPR00903; Pept_Ser_Cys
Db	261	IIFTIPIFIILIFIMPLPLKGSSL---GRGENYRGTVSUTASKTCQRMWSBOTPHRN 316	DR	InterPro; IPR01254; Pept_Didae_SIA.
Oy	212	RYPENPKQLDENYCRPDKGKAAPWCHTNQSQRWECKISQDSS 258	DR	InterPro; IPR01314; Peptidase_SIA_pr.
Db	317	RTPENFPCQNLEENYCRNPDGETARPWCYTDSQRLMEYCEIPSOGSS 363	DR	Pfam; PF0051; Kringle_5.
RESULT 11				
PLMN_MACEU	ID	PLMN_MACEU	STANDARD;	PRT;
	AC	018783;		806 AA.
	DT	25-OT-2004 (Rel. 45, Created)		
	DT	25-OT-2004 (Rel. 45, Last sequence update)		
	DT	25-OT-2004 (Rel. 45, Last annotation update)		
	DE	Plasminogen precursor (EC 3.4.21.7).		
	GN	Name=PLUG;		
	OS	Macropus_eugenii (Tanner wallaby).		
	OC	Bukaritota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	OC	Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.		
	NCBI_TaxID	9315;		
	RN	[1]		
RP	SEQUENCE FROM N.A.			
TX	TISSUE=Liver;			
RA	MEDLINE=98004511; PubMed=9342350; DOI=10.1073/pnas.94.22.11992;			
RA	Lawn R.M., Schwartz K., Piatthy L.;			
RT	"Convergent evolution of apolipoprotein(a) in primates and hedgehog."			
RL	Proc. Natl. Acad. Sci. U.S.A. 94:11982-11997(1997).			
CC	-!- FUNCTION: Plasmin dissolves the fibrin of blood clots and acts as a proteolytic factor in a variety of other processes including embryonic development, tissue remodeling, tumor invasion, and inflammation. In ovulation it weakens the walls of the Graafian follicle. It activates the urokinase-type plasminogen activator, collagenases and several complement zymogens, such as C1 and C5. It cleaves fibrin, fibronectin, thrombospondin, laminin and von Willebrand factor (By similarity).			
CC	-!- CATALYTIC ACTIVITY: Preferential cleavage: Lys- Xaa > Arg- Xaa; higher selectivity than trypsin. Converts fibrin into soluble products.			
CC	-!- ENZYME REGULATION: Converted into plasmin by plasminogen activators, both plasminogen and its activator being bound to fibrin. Activated with catalytic amounts of streptokinase (By similarity).			
CC	-!- SUBCELLULAR LOCATION: Secreted.			
CC	-!- MISCELLANEOUS: Plasmin is inactivated by alpha-2-antiplasmin immediately after dissociation from the clot (By similarity).			
CC	-!- MISCELLANEOUS: In the presence of the inhibitor, the activation involves only cleavage after Arg-576, resulting in 2 chains held together by 2 disulfide bonds. Without the inhibitor, the activation involves also removal of the activation peptide (By similarity).			
CC	-!- SIMILARITY: Belongs to the peptidase S1 family. Plasminogen subfamily. Contains 5 kringle domains.			
CC	-!- SIMILARITY: Contains 1 PAN domain.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
DR	EMBL; AF012297; AAB65760.1; -.			
DR	HSSP; P00747; BUL.			
DR	MEROPS; S01_233; -.			
DR	InterPro; IPR000001; Kringle.			
DR	InterPro; IPR03014; PAN.			
DR	InterPro; IPR03609; Pan_app.			
DR	PFam; PF00051; Kringle_5.			
DR	Pfam; PF00024; PAN; 1.			
DR	DR	DR	DR	DR
DR	Pfam; PF00089; Trypsin; 1.			
DR	PRSF; PINS00150; Plasmin; 1.			
DR	PRINTS; PRO0722; CHMNOTRIPSIN.			
DR	PRINTS; PRO0018; KRINGLE.			
DR	PRINTS; PRO1505; PROTHROMBIN.			
DR	PRODOM; PDD00395; Kringle_5.			
DR	SMART; SM00130; KR; 5.			
DR	SMART; SM00473; PAN_AP; 1.			
DR	SMART; SM00020; TRY_P; SPC; 1.			
DR	PROSITE; PSS0021; KRINGLE_1; 5.			
DR	PROSITE; PSS0070; KRINGLE_2; 5.			
DR	PROSITE; PSS0948; PAN; 1.			
DR	PROSITE; PS50240; TRYPSIN_DOM; 1.			
DR	PROSITE; PS00134; TRYPSIN_HIS; 1.			
KW	Blood coagulation; Fibrinolysis; Glycoprotein; Hydrolase; Kringle; Plasma; Repeat; Serine protease; Signal; Tissue remodeling; Zymogen.			
FT	SIGNAL	1	19	Potential.
FT	CHAIN	20	806	
FT	CHAIN	20	567	
FT	PEPTIDE	20	96	
FT	CHAIN	97	576	
FT	CHAIN	577	806	
FT	DOMAIN	20	98	
FT	DOMAIN	102	181	
FT	DOMAIN	184	262	
FT	DOMAIN	274	352	
FT	DOMAIN	370	448	
FT	DOMAIN	475	555	
FT	DOMAIN	577	806	
FT	ACT_SITE	618	618	
FT	ACT_SITE	661	661	
FT	ACT_SITE	755	755	
FT	DISUFID	49	73	
FT	DISUFID	53	61	
FT	DISUFID	103	181	
FT	DISUFID	124	164	
FT	DISUFID	152	176	
FT	DISUFID	185	262	
FT	DISUFID	188	316	
FT	DISUFID	206	245	
FT	DISUFID	234	257	
FT	DISUFID	275	352	
FT	DISUFID	296	335	
FT	DISUFID	324	347	
FT	DISUFID	371	448	
FT	DISUFID	392	431	
FT	DISUFID	420	443	
FT	DISUFID	476	555	
FT	DISUFID	497	538	
FT	DISUFID	526	550	
FT	DISUFID	563	681	
FT	DISUFID	573	581	
FT	DISUFID	603	619	
FT	DISUFID	695	762	
FT	DISUFID	725	741	
FT	DISUFID	752	780	
SO	SEQUENCE	806 AA;	90980 MW;	95FAA86DC20064D5 CRC64;
Query Match	75.3%	Score 1160; DB 1; Length 806;		
Best Local Similarity	71.7%	Pred. No. 4e-80; Gaps 0;		
Matches	185	Conservative 34; Mismatches 39; Indels 0;		
DR	1 VYLLBACKTGNGKNTGTMKNGTCKOMNSSPHRPRSPATHPSGCLEBNYCNRNND	60		

Db 98 IYLSDCKSGNGNRGRFLSKTMSGITCQKNDLSPHPVNPNTAPSXVFDAGLEKNYCRNPPD 157^{*}
 DR InterPro; IPR003014; PAN.
 Qy 61 DPOGPMWCYTTPPEKRYDCIDELCEBECMHSGENGDGKISKTMGLEGACAWDSOSPHAH 120
 DR InterPro; IPR003609; Pan.apb.
 Db 158 DVKGPCYCCTTMDIREKVDPECEBECMGSGENVRGTISKTESGICOPWDQSOPBHSH 217
 DR InterPro; IPR001254; Peptidase_SIA.
 DR InterPro; IPR001314; Peptidase_SIA.
 DR InterPro; IPR003966; Peptidase_SIA_Dr.
 DR InterPro; IPR0003; Pept_Ser_Cys.
 DR Pfam; PF00051; Kringle; 5.
 DR Pfam; PF00024; PAN; 1.
 DR Pfam; PF0089; Trypsin; 1.
 DR PRINTS; PRO0722; CHYMOTRYPSIN.
 DR PRINTS; PRO0018; KRINGLE.
 DR PRINTS; PRO1505; PROTHROMBIN.
 DR ProDom; PDD00395; Kringle; 5.
 DR SMART; SM00130; KR; 5.
 DR SMART; SM00473; PAN_AP; 1.
 DR SMART; SM00020; TRY_SPC; 1.
 DR PROSITE; PS00021; KRINGLE; 1; 3.
 DR PROSITE; PS00070; KRINGLE; 2; 5.
 DR PROSITE; PS50948; PAN; 1.
 DR PROSITE; PS00241; TRIPSIN_DOM; 1.
 AC 06PBA6^{*} PRELIMINARY; PRT; 818 AA.
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DB 05-JUL-2004 (TREMBLrel. 27, last annotation update)
 GN Name=plg;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Danio.
 OX NCBI_TAXID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=22388257; PubMed=12479732; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Fingold E.A., Grouse L.H., Detje J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Sheinman C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaeffer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Mardisera K., Farmer A., Rubin G.M., Hong L.,
 RA Stapleton M., Soakes M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange T.B.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Milliany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villain D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahney J., Heitman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shvchenko Y., Boutefaud G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.",
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA Strausberg R.;
 RL Submitted (Oct-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC05901; AAH59801.1; -.
 DR HSSP; P00747; 1B21.
 DR ZFIN; ZDB-GENE-030131-411; plg.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0003809; F:thrombin activity; IEA..
 DR GO; GO:0004295; F:trypsin activity; IEA.
 DR GO; GO:0007596; P:blood coagulation; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR000001; Kringle.

RESULT 12

Q6PBA6 PRELIMINARY; PRT; 818 AA.

AC 06PBA6^{*} PRELIMINARY; PRT; 818 AA.

DT 05-JUL-2004 (TREMBLrel. 27, Created)

DB 05-JUL-2004 (TREMBLrel. 27, last annotation update)

GN Name=plg;

OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Danio.
 OX NCBI_TAXID=7955;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Embryo;

RX MEDLINE=22388257; PubMed=12479732; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Fingold E.A., Grouse L.H., Detje J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Sheinman C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaeffer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diachenko L., Mardisera K., Farmer A., Rubin G.M., Hong L.,
 RA Stapleton M., Soakes M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange T.B.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Milliany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villain D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahney J., Heitman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shvchenko Y., Boutefaud G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Jones S.J., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.",
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Embryo;

RQ Submitted (Oct-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC05901; AAH59801.1; -.

DR HSSP; P00747; 1B21.

DR ZFIN; ZDB-GENE-030131-411; plg.

DR GO; GO:0005509; F:calcium ion binding; IEA.

DR GO; GO:0004263; F:chymotrypsin activity; IEA.

DR GO; GO:0008233; F:peptidase activity; IEA.

DR GO; GO:0003809; F:thrombin activity; IEA..

DR GO; GO:0004295; F:trypsin activity; IEA.

DR GO; GO:0007596; P:blood coagulation; IEA.

DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

DR InterPro; IPR000001; Kringle.

RESULT 13

Q8398 PRELIMINARY; PRT; 2869 AA.

ID Q28398^{*} PRELIMINARY; PRT; 2869 AA.

AC 028398^{*} PRELIMINARY; PRT; 2869 AA.

DT 01-NOV-1995 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)

DT 01-MAR-2004 (TREMBLrel. 26, last annotation update)

DB Apolipoprotein(A) (Fragment).

OS Erinaceus europaeus (Western European hedgehog).

OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Insectivora; Erinaceidae; Erinaceinae; Erinaceus.

OC NCBI_TAXID=9365;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Liver;

RQ MEDLINE=96025778; PubMed=7592597; DOI=10.1074/jbc.270.41.24004;

RA Byrne C.D., Fong K.J., Meir K., Patchy L., Wade D.P.,
 RA Byrne C.D., Fong K.J., Meir K., Patchy L., Wade D.P.,
 RA The recurring evolution of lipoprotein(a). Insights from cloning of
 RA hedgehog apolipoprotein(a);
 RA J. Biol. Chem. 270:24004-24009(1995).

RL U33170; AAC48222.1; -.

DR EMBL; T18518; T18518.

OC
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
 OX Xenopodinae; Xeropusp.
 RN NCBI_TAXID=8355;
 RL [1]
 RP SEQUENCE FROM N.A.
 RA Ruiz I Alcalde A.; Terry C.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U57155; AAB52174.1; -.
 DR HSSP; P00746; 1FDP.
 DR GO; GO:0005509; F:calcium ion binding; IEA.
 DR GO; GO:0004263; F:chymotrypsin activity; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 DR GO; GO:0003809; F:thrombin activity; IEA.
 DR GO; GO:000759; P:blood coagulation; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR Pfam; PF0051; Kringle; 4.
 DR Pfam; PF0024; PAN; 1.
 DR Pfam; PF0089; Trypsin; 1.
 DR PIRSF; PIISF001152; HGF MST1; 1.
 DR PRINTS; PR00722; CHYMOTRYPsin.
 DR PRINTS; PR00018; KRINGLE.
 DR PROSITE; PS0005; PROTHROMBIN.
 DR PROSITE; PS0035; Kringle; 4.
 DR SMART; SMD0130; KR; 4.
 DR SMART; SMD0473; PAN_AP; 1.
 DR SMART; SMD0020; TTP_SPC; 1.
 DR PROSITE; PS00021; KRINGLE_1; 4.
 DR PROSITE; PS50070; KRINGLE_2; 4.
 DR PROSITE; PS50948; PAN; 1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR HYDROLASE; Kringle; Protease; Serine protease.
 SQ SEQUENCE: 716 AA; 81971 MW; 50376A0E4398798 CRC64;

40% + 70%

Query Match 52.6%; Score 809.5; DB 2; Length 716;
 Best Local Similarity 54.9%; Pred. No. 1.8e-53; Indels 5; Gaps 4;
 Matches 141; Conservative 28; Mismatches 83; InDel 5;

Qy	2	YLSBECKTGNSKVKYRGTMKSITKGITCQKWSSTSPHRPRSPATPHSEGLENTRANPOND	61
Db	114	Y : : : 180 KGTGENYGRNVAVTGSGTQHWSQTPTHTERI PENFCKNLDENYCRNDGKAPWCH 239 292 KERGEGRGKNTTTSIGRCORWSDTPOSHFLPEKYPCKGLDENYCNPDGSEAPCF 351 Qy 240 TNSQRWEC-KPSC 255 Db 352 TLPGMRMAYCFOQRC 369	

Search completed: July 27, 2005, 03:30:09
 Job time : 63 secs